GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: September 9, 2004, 10:53:58 ; Search time 53.0897 Seconds
(without alignments)
654.615 Million cell updates/sec

Title: US-09-880-748-2_COPY_1_123
Perfect score: 640
Sequence: 1 QVQLQQSGAEVKKPGSSVRV.....LFPHYGMDVWGRGTMVTVSS 123

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

[redacted]l number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 70 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
[redacted] 1	640	100.0	246	5	ABP44917	Abp44917 Human BLy
2	640	100.0	249	5	ABP44468	Abp44468 Human BLy
3	640	100.0	249	5	ABP43991	Abp43991 Human BLy
4	640	100.0	249	5	ABP44708	Abp44708 Human BLy
5	640	100.0	249	5	ABP44460	Abp44460 Human BLy
6	640	100.0	249	5	ABP44785	Abp44785 Human BLy
7	640	100.0	249	5	ABP44607	Abp44607 Human BLy
8	637	99.5	246	5	ABP45415	Abp45415 Human BLy
9	637	99.5	246	5	ABP45770	Abp45770 Human BLy
10	637	99.5	249	5	ABP44602	Abp44602 Human BLy
11	634	99.1	249	5	ABP44688	Abp44688 Human BLy
12	634	99.1	249	5	ABP45737	Abp45737 Human BLy
13	633	98.9	246	5	ABP45297	Abp45297 Human BLy
14	632	98.8	249	5	ABP44677	Abp44677 Human BLy
15	632	98.8	249	5	ABP44313	Abp44313 Human BLy
16	631	98.6	246	5	ABP45807	Abp45807 Human BLy
17	631	98.6	249	5	ABP44710	Abp44710 Human BLy
18	626	97.8	249	5	ABP44775	Abp44775 Human BLy
19	626	97.8	249	5	ABP44783	Abp44783 Human BLy
20	626	97.8	249	5	ABP44793	Abp44793 Human BLy
21	623	97.3	249	5	ABP44314	Abp44314 Human BLy
22	623	97.3	249	5	ABP44750	Abp44750 Human BLy
23	623	97.3	249	5	ABP44804	Abp44804 Human BLy
24	621	97.0	249	5	ABP44450	Abp44450 Human BLy
25	621	97.0	249	5	ABP44800	Abp44800 Human BLy
26	621	97.0	249	5	ABP44763	Abp44763 Human BLy
27	621	97.0	249	5	ABP44311	Abp44311 Human BLy
28	621	97.0	249	5	ABP44815	Abp44815 Human BLy
29	621	97.0	249	5	ABP44741	Abp44741 Human BLy
30	621	97.0	249	5	ABP44318	Abp44318 Human BLy
31	621	97.0	249	5	ABP44781	Abp44781 Human BLy
32	621	97.0	249	5	ABP44786	Abp44786 Human BLy
33	621	97.0	249	5	ABP44797	Abp44797 Human BLy
34	621	97.0	249	5	ABP44814	Abp44814 Human BLy
35	621	97.0	249	5	ABP44733	Abp44733 Human BLy
36	620	96.9	249	5	ABP44522	Abp44522 Human BLy
37	620	96.9	249	5	ABP44698	Abp44698 Human BLy
38	620	96.9	249	5	ABP44718	Abp44718 Human BLy
39	619	96.7	249	5	ABP44787	Abp44787 Human BLy
40	619	96.7	249	5	ABP44803	Abp44803 Human BLy
41	618	96.6	249	5	ABP44561	Abp44561 Human BLy
42	618	96.6	249	5	ABP44680	Abp44680 Human BLy
43	618	96.6	249	5	ABP44687	Abp44687 Human BLy
44	618	96.6	249	5	ABP44690	Abp44690 Human BLy
45	618	96.6	249	5	ABP44777	Abp44777 Human BLy
46	618	96.6	249	5	ABP44731	Abp44731 Human BLy
47	617	96.4	249	5	ABP44794	Abp44794 Human BLy
48	617	96.4	249	5	ABP44434	Abp44434 Human BLy
49	617	96.4	249	5	ABP44801	Abp44801 Human BLy
50	617	96.4	249	5	ABP44639	Abp44639 Human BLy
51	617	96.4	249	5	ABP44684	Abp44684 Human BLy
52	617	96.4	249	5	ABP44416	Abp44416 Human BLy
53	617	96.4	249	5	ABP44762	Abp44762 Human BLy
54	616	96.2	249	5	ABP44809	Abp44809 Human BLy
55	616	96.2	249	5	ABP44759	Abp44759 Human BLy
56	616	96.2	249	5	ABP44663	Abp44663 Human BLy
57	616	96.2	249	5	ABP44310	Abp44310 Human BLy
58	616	96.2	249	5	ABP44580	Abp44580 Human BLy
59	615	96.1	249	5	ABP44817	Abp44817 Human BLy
60	615	96.1	249	5	ABP44572	Abp44572 Human BLy
61	615	96.1	249	5	ABP44717	Abp44717 Human BLy
62	615	96.1	249	5	ABP44792	Abp44792 Human BLy
63	615	96.1	249	5	ABP44605	Abp44605 Human BLy
64	614	95.9	249	5	ABP44745	Abp44745 Human BLy
65	614	95.9	249	5	ABP44776	Abp44776 Human BLy
66	614	95.9	249	5	ABP44636	Abp44636 Human BLy
67	614	95.9	249	5	ABP44780	Abp44780 Human BLy
68	614	95.9	249	5	ABP44819	Abp44819 Human BLy
69	614	95.9	249	5	ABP44779	Abp44779 Human BLy
70	614	95.9	249	5	ABP44702	Abp44702 Human BLy

ALIGNMENTS

RESULT 1
ABP44917
ID ABP44917 standard; protein; 246 AA.
XX
AC ABP44917;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human BLyS binding scFv SEQ ID 928.
XX
KW BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS Homo sapiens.
XX
PN WO200202641-A1.
XX
PD 10-JAN-2002.
XX

PF 15-JUN-2001; 2001WO-US019110.
XX
PR 16-JUN-2000; 2000US-0212210P.
PR 17-OCT-2000; 2000US-0240816P.
PR 16-MAR-2001; 2001US-0276248P.
PR 21-MAR-2001; 2001US-0277379P.
PR 25-MAY-2001; 2001US-0293499P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX
DR WPI; 2002-114799/15.
XX
PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
PT diagnosis and treatment of cancers and immune disorders.
XX
PS Claim 1; Page 1509-1510; 3148pp; English.
XX
CC This invention describes novel antibodies that immunospecifically bind to
CC B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of BLyS. The antibodies bind to BLyS
CC and so may be used to detect and quantitate the presence of BLyS in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of BLyS. They may also be
CC administered to treat diseases associated with aberrant BLyS expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention
XX
SQ Sequence 246 AA;

Query Match 100.0%; Score 640; DB 5; Length 246;
Best Local Similarity 100.0%; Pred. No. 9.8e-52;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60

          61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHYGMDVWGRGTMVT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHYGMDVWGRGTMVT 120

Qy        121 VSS 123
              |||
Db        121 VSS 123
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RESULT 2
ABP44468
ID ABP44468 standard; protein; 249 AA.
XX
AC ABP44468;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human BLyS binding scFv SEQ ID 479.
XX
KW BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS Homo sapiens.
XX
PN WO200202641-A1.
XX
PD 10-JAN-2002.
XX
PF 15-JUN-2001; 2001WO-US019110.
XX
PR 16-JUN-2000; 2000US-0212210P.
PR 17-OCT-2000; 2000US-0240816P.
PR 16-MAR-2001; 2001US-0276248P.
PR 21-MAR-2001; 2001US-0277379P.
PR 25-MAY-2001; 2001US-0293499P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX
DR WPI; 2002-114799/15.
XX
PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
PT diagnosis and treatment of cancers and immune disorders.
XX
PS Claim 1; Page 974-975; 3148pp; English.
XX
CC This invention describes novel antibodies that immunospecifically bind to
CC B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of BLyS. The antibodies bind to BLyS
CC and so may be used to detect and quantitate the presence of BLyS in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of BLyS. They may also be
CC administered to treat diseases associated with aberrant BLyS expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention
XX
SQ Sequence 249 AA;

Query Match 100.0%; Score 640; DB 5; Length 249;
Best Local Similarity 100.0%; Pred. No. 9.9e-52;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60

Qy         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHYGMDVWGRGTMVT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHYGMDVWGRGTMVT 120

Qy        121 VSS 123
              |||
Db        121 VSS 123
```

RESULT 3
ABP43991
ID ABP43991 standard; protein; 249 AA.
XX
AC ABP43991;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human BLyS binding scFv SEQ ID 2.

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XX
KW   BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW   tumour necrosis factor; B cell proliferation; B cell differentiation;
KW   immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW   antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW   systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW   common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS   Homo sapiens.
XX
PN   WO200202641-A1.
XX
PD   10-JAN-2002.
XX
PF   15-JUN-2001; 2001WO-US019110.
XX
PR   16-JUN-2000; 2000US-0212210P.
PR   17-OCT-2000; 2000US-0240816P.
PR   16-MAR-2001; 2001US-0276248P.
PR   21-MAR-2001; 2001US-0277379P.
PR   25-MAY-2001; 2001US-0293499P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
PA   (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI   Ruben SM,  Barash SC,  Choi GH,  Vaughan T,  Hilbert D;
XX
DR   WPI; 2002-114799/15.
XX
PT   Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
PT   diagnosis and treatment of cancers and immune disorders.
XX
PS   Claim 1; Page 408-409; 3148pp; English.
XX
CC   This invention describes novel antibodies that immunospecifically bind to
CC   B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the
CC   tumour necrosis factor (TNF) super family and induces B cell
CC   proliferation and differentiation. The antibodies of the invention have
CC   cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC   antirheumatic and antiAIDS activity and can be used in vaccines to
CC   inhibit the expression and activity of BLyS. The antibodies bind to BLyS
CC   and so may be used to detect and quantitate the presence of BLyS in
CC   biological samples and may be used in this way to diagnose disease
CC   associated with aberrant expression of BLyS. They may also be
CC   administered to treat diseases associated with aberrant BLyS expression
CC   and activity such as cancer, immune, and autoimmune disorders and
CC   diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC   immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC   acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC   the antibodies and fragments of the antibodies described in the method of
CC   the invention
XX
SQ   Sequence 249 AA;

  Query Match          100.0%;  Score 640;  DB 5;  Length 249;
  Best Local Similarity  100.0%;  Pred. No. 9.9e-52;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60

Qy         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHYGMDVWGRGTMVT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHYGMDVWGRGTMVT 120

Qy        121 VSS 123
              |||
Db        121 VSS 123


RESULT 4
ABP44708
ID   ABP44708 standard; protein; 249 AA.
XX
AC   ABP44708;
XX
DT   19-AUG-2002  (first entry)
XX
DE   Human BLyS binding scFv SEQ ID 719.
XX
KW   BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW   tumour necrosis factor; B cell proliferation; B cell differentiation;
KW   immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW   antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW   systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW   common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS   Homo sapiens.
XX
PN   WO200202641-A1.
XX
PD   10-JAN-2002.
XX
PF   15-JUN-2001; 2001WO-US019110.
XX
PR   16-JUN-2000; 2000US-0212210P.
PR   17-OCT-2000; 2000US-0240816P.
PR   16-MAR-2001; 2001US-0276248P.
PR   21-MAR-2001; 2001US-0277379P.
PR   25-MAY-2001; 2001US-0293499P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
PA   (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI   Ruben SM,  Barash SC,  Choi GH,  Vaughan T,  Hilbert D;
XX
DR   WPI; 2002-114799/15.
XX
PT   Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
PT   diagnosis and treatment of cancers and immune disorders.
XX
PS   Claim 1; Page 1259-1260; 3148pp; English.
XX
CC   This invention describes novel antibodies that immunospecifically bind to
CC   B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the
CC   tumour necrosis factor (TNF) super family and induces B cell
CC   proliferation and differentiation. The antibodies of the invention have
CC   cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC   antirheumatic and antiAIDS activity and can be used in vaccines to
CC   inhibit the expression and activity of BLyS. The antibodies bind to BLyS
CC   and so may be used to detect and quantitate the presence of BLyS in
CC   biological samples and may be used in this way to diagnose disease
CC   associated with aberrant expression of BLyS. They may also be
CC   administered to treat diseases associated with aberrant BLyS expression
CC   and activity such as cancer, immune, and autoimmune disorders and
CC   diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC   immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC   acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC   the antibodies and fragments of the antibodies described in the method of
CC   the invention
XX
SQ   Sequence 249 AA;

  Query Match          100.0%;  Score 640;  DB 5;  Length 249;
  Best Local Similarity  100.0%;  Pred. No. 9.9e-52;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60

Qy         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHYGMDVWGRGTMVT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHYGMDVWGRGTMVT 120
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```
Qy        121 VSS 123
              |||
Db        121 VSS 123


RESULT 5
ABP44460
ID   ABP44460 standard; protein; 249 AA.
XX
AC   ABP44460;
XX
DT   19-AUG-2002  (first entry)
XX
DE   Human BLyS binding scFv SEQ ID 471.
XX
KW   BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW   tumour necrosis factor; B cell proliferation; B cell differentiation;
KW   immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW   antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW   systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW   common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS   Homo sapiens.
XX
PN   WO200202641-A1.
XX
PD   10-JAN-2002.
XX
PF   15-JUN-2001; 2001WO-US019110.
XX
PR   16-JUN-2000; 2000US-0212210P.
PR   17-OCT-2000; 2000US-0240816P.
PR   16-MAR-2001; 2001US-0276248P.
PR   21-MAR-2001; 2001US-0277379P.
PR   25-MAY-2001; 2001US-0293499P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
PA   (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI   Ruben SM,  Barash SC,  Choi GH,  Vaughan T,  Hilbert D;
XX
DR   WPI; 2002-114799/15.
XX
PT   Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
PT   diagnosis and treatment of cancers and immune disorders.
XX
PS   Claim 1; Page 965-966; 3148pp; English.
XX
CC   This invention describes novel antibodies that immunospecifically bind to
CC   B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the
CC   tumour necrosis factor (TNF) super family and induces B cell
CC   proliferation and differentiation. The antibodies of the invention have
CC   cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC   antirheumatic and antiAIDS activity and can be used in vaccines to
CC   inhibit the expression and activity of BLyS. The antibodies bind to BLyS
CC   and so may be used to detect and quantitate the presence of BLyS in
CC   biological samples and may be used in this way to diagnose disease
CC   associated with aberrant expression of BLyS. They may also be
CC   administered to treat diseases associated with aberrant BLyS expression
CC   and activity such as cancer, immune, and autoimmune disorders and
CC   diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC   immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC   acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC   the antibodies and fragments of the antibodies described in the method of
CC   the invention
XX
SQ   Sequence 249 AA;

  Query Match           100.0%;  Score 640;  DB 5;  Length 249;
  Best Local Similarity  100.0%;  Pred. No. 9.9e-52;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60

Qy         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHYGMDVWGRGTMVT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHYGMDVWGRGTMVT 120

Qy        121 VSS 123
              |||
Db        121 VSS 123


RESULT 6
ABP44785
ID   ABP44785 standard; protein; 249 AA.
XX
AC   ABP44785;
XX
DT   19-AUG-2002  (first entry)
XX
DE   Human BLyS binding scFv SEQ ID 796.
XX
KW   BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW   tumour necrosis factor; B cell proliferation; B cell differentiation;
KW   immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW   antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW   systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW   common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS   Homo sapiens.
XX
PN   WO200202641-A1.
XX
PD   10-JAN-2002.
XX
PF   15-JUN-2001; 2001WO-US019110.
XX
PR   16-JUN-2000; 2000US-0212210P.
PR   17-OCT-2000; 2000US-0240816P.
PR   16-MAR-2001; 2001US-0276248P.
PR   21-MAR-2001; 2001US-0277379P.
PR   25-MAY-2001; 2001US-0293499P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
PA   (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI   Ruben SM,  Barash SC,  Choi GH,  Vaughan T,  Hilbert D;
XX
DR   WPI; 2002-114799/15.
XX
PT   Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
PT   diagnosis and treatment of cancers and immune disorders.
XX
PS   Claim 1; Page 1351-1352; 3148pp; English.
XX
CC   This invention describes novel antibodies that immunospecifically bind to
CC   B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the
CC   tumour necrosis factor (TNF) super family and induces B cell
CC   proliferation and differentiation. The antibodies of the invention have
CC   cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC   antirheumatic and antiAIDS activity and can be used in vaccines to
CC   inhibit the expression and activity of BLyS. The antibodies bind to BLyS
CC   and so may be used to detect and quantitate the presence of BLyS in
CC   biological samples and may be used in this way to diagnose disease
CC   associated with aberrant expression of BLyS. They may also be
CC   administered to treat diseases associated with aberrant BLyS expression
CC   and activity such as cancer, immune, and autoimmune disorders and
CC   diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC   immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC   acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC   the antibodies and fragments of the antibodies described in the method of
CC   the invention
XX
```

```
SQ   Sequence 249 AA;

  Query Match             100.0%;  Score 640;  DB 5;  Length 249;
  Best Local Similarity   100.0%;  Pred. No. 9.9e-52;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60

Qy         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHYGMDVWGRGTMVT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHYGMDVWGRGTMVT 120

Qy        121 VSS 123
              |||
Db        121 VSS 123


RESULT 7
[redacted]4607
ID   ABP44607 standard; protein; 249 AA.
XX
AC   ABP44607;
XX
DT   19-AUG-2002  (first entry)
XX
DE   Human BLyS binding scFv SEQ ID 618.
XX
KW   BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW   tumour necrosis factor; B cell proliferation; B cell differentiation;
KW   immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW   antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW   systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW   common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS   Homo sapiens.
XX
PN   WO200202641-A1.
XX
PD   10-JAN-2002.
XX
PF   15-JUN-2001; 2001WO-US019110.
XX
PR   16-JUN-2000; 2000US-0212210P.
PR   17-OCT-2000; 2000US-0240816P.
PR   16-MAR-2001; 2001US-0276248P.
PR   21-MAR-2001; 2001US-0277379P.
PR   25-MAY-2001; 2001US-0293499P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
PA   (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI   Ruben SM,  Barash SC,  Choi GH,  Vaughan T,  Hilbert D;
XX
DR   WPI; 2002-114799/15.
XX
PT   Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
PT   diagnosis and treatment of cancers and immune disorders.
XX
PS   Claim 1; Page 1139-1140; 3148pp; English.
XX
CC   This invention describes novel antibodies that immunospecifically bind to
CC   B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the
CC   tumour necrosis factor (TNF) super family and induces B cell
CC   proliferation and differentiation. The antibodies of the invention have
CC   cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC   antirheumatic and antiAIDS activity and can be used in vaccines to
CC   inhibit the expression and activity of BLyS. The antibodies bind to BLyS
CC   and so may be used to detect and quantitate the presence of BLyS in
CC   biological samples and may be used in this way to diagnose disease
CC   associated with aberrant expression of BLyS. They may also be
CC   administered to treat diseases associated with aberrant BLyS expression
CC   and activity such as cancer, immune, and autoimmune disorders and
CC   diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC   immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC   acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC   the antibodies and fragments of the antibodies described in the method of
CC   the invention
XX
SQ   Sequence 249 AA;

  Query Match             100.0%;  Score 640;  DB 5;  Length 249;
  Best Local Similarity   100.0%;  Pred. No. 9.9e-52;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60

Qy         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHYGMDVWGRGTMVT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHYGMDVWGRGTMVT 120

Qy        121 VSS 123
              |||
Db        121 VSS 123


RESULT 8
ABP45415
ID   ABP45415 standard; protein; 246 AA.
XX
AC   ABP45415;
XX
DT   19-AUG-2002  (first entry)
XX
DE   Human BLyS binding scFv SEQ ID 1426.
XX
KW   BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW   tumour necrosis factor; B cell proliferation; B cell differentiation;
KW   immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW   antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW   systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW   common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS   Homo sapiens.
XX
PN   WO200202641-A1.
XX
PD   10-JAN-2002.
XX
PF   15-JUN-2001; 2001WO-US019110.
XX
PR   16-JUN-2000; 2000US-0212210P.
PR   17-OCT-2000; 2000US-0240816P.
PR   16-MAR-2001; 2001US-0276248P.
PR   21-MAR-2001; 2001US-0277379P.
PR   25-MAY-2001; 2001US-0293499P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
PA   (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI   Ruben SM,  Barash SC,  Choi GH,  Vaughan T,  Hilbert D;
XX
DR   WPI; 2002-114799/15.
XX
PT   Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
PT   diagnosis and treatment of cancers and immune disorders.
XX
PS   Claim 1; Page 2104-2105; 3148pp; English.
XX
CC   This invention describes novel antibodies that immunospecifically bind to
CC   B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the
CC   tumour necrosis factor (TNF) super family and induces B cell
CC   proliferation and differentiation. The antibodies of the invention have
```

```
CC   cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC   antirheumatic and antiAIDS activity and can be used in vaccines to
CC   inhibit the expression and activity of BLyS. The antibodies bind to BLyS
CC   and so may be used to detect and quantitate the presence of BLyS in
CC   biological samples and may be used in this way to diagnose disease
CC   associated with aberrant expression of BLyS. They may also be
CC   administered to treat diseases associated with aberrant BLyS expression
CC   and activity such as cancer, immune, and autoimmune disorders and
CC   diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC   immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC   acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC   the antibodies and fragments of the antibodies described in the method of
CC   the invention
XX
SQ   Sequence 246 AA;

  Query Match             99.5%;  Score 637;  DB 5;  Length 246;
  Best Local Similarity   99.2%;  Pred. No. 1.9e-51;
  Matches  122;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60

Qy         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHYGMDVWGRGTMVT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:||
Db         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHYGMDVWGRGTLVT 120

Qy        121 VSS 123
              |||
Db        121 VSS 123


RESULT 9
ABP45770
ID   ABP45770 standard; protein; 246 AA.
XX
AC   ABP45770;
XX
DT   19-AUG-2002  (first entry)
XX
DE   Human BLyS binding scFv SEQ ID 1781.
XX
KW   BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW   tumour necrosis factor; B cell proliferation; B cell differentiation;
KW   immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW   antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW   systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW   common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS   Homo sapiens.
XX
PN   WO200202641-A1.
XX
PD   10-JAN-2002.
XX
PF   15-JUN-2001; 2001WO-US019110.
XX
PR   16-JUN-2000; 2000US-0212210P.
PR   17-OCT-2000; 2000US-0240816P.
PR   16-MAR-2001; 2001US-0276248P.
PR   21-MAR-2001; 2001US-0277379P.
PR   25-MAY-2001; 2001US-0293499P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
PA   (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI   Ruben SM,  Barash SC,  Choi GH,  Vaughan T,  Hilbert D;
XX
DR   WPI; 2002-114799/15.
XX
PT   Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
PT   diagnosis and treatment of cancers and immune disorders.
XX
PS   Claim 1; Page 2527-2528; 3148pp; English.
XX
CC   This invention describes novel antibodies that immunospecifically bind to
CC   B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the
CC   tumour necrosis factor (TNF) super family and induces B cell
CC   proliferation and differentiation. The antibodies of the invention have
CC   cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC   antirheumatic and antiAIDS activity and can be used in vaccines to
CC   inhibit the expression and activity of BLyS. The antibodies bind to BLyS
CC   and so may be used to detect and quantitate the presence of BLyS in
CC   biological samples and may be used in this way to diagnose disease
CC   associated with aberrant expression of BLyS. They may also be
CC   administered to treat diseases associated with aberrant BLyS expression
CC   and activity such as cancer, immune, and autoimmune disorders and
CC   diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC   immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC   acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC   the antibodies and fragments of the antibodies described in the method of
CC   the invention
XX
SQ   Sequence 246 AA;

  Query Match             99.5%;  Score 637;  DB 5;  Length 246;
  Best Local Similarity   99.2%;  Pred. No. 1.9e-51;
  Matches  122;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60

Qy         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHYGMDVWGRGTMVT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:||
Db         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHYGMDVWGRGTLVT 120

Qy        121 VSS 123
              |||
Db        121 VSS 123


RESULT 10
ABP44602
ID   ABP44602 standard; protein; 249 AA.
XX
AC   ABP44602;
XX
DT   19-AUG-2002  (first entry)
XX
DE   Human BLyS binding scFv SEQ ID 613.
XX
KW   BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW   tumour necrosis factor; B cell proliferation; B cell differentiation;
KW   immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW   antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW   systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW   common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS   Homo sapiens.
XX
PN   WO200202641-A1.
XX
PD   10-JAN-2002.
XX
PF   15-JUN-2001; 2001WO-US019110.
XX
PR   16-JUN-2000; 2000US-0212210P.
PR   17-OCT-2000; 2000US-0240816P.
PR   16-MAR-2001; 2001US-0276248P.
PR   21-MAR-2001; 2001US-0277379P.
PR   25-MAY-2001; 2001US-0293499P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
PA   (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
```

XX
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX
DR WPI; 2002-114799/15.
XX
PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
PT diagnosis and treatment of cancers and immune disorders.
XX
PS Claim 1; Page 1133-1134; 3148pp; English.
XX
CC This invention describes novel antibodies that immunospecifically bind to
CC B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of BLyS. The antibodies bind to BLyS
CC and so may be used to detect and quantitate the presence of BLyS in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of BLyS. They may also be
CC administered to treat diseases associated with aberrant BLyS expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention
XX
SQ Sequence 249 AA;

Query Match 99.5%; Score 637; DB 5; Length 249;
Best Local Similarity 99.2%; Pred. No. 1.9e-51;
Matches 122; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60

Qy 61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHYGMDVWGRGTMVT 120
||||||||||||||||||||||||||||||:||||||||||||||||||||||||||||
Db 61 SQNFQGRVAITADESTSTASMELSSLRSEDTAMYYCARSRDLLLFPHYGMDVWGRGTMVT 120

Qy 121 VSS 123
|||
Db 121 VSS 123

RESULT 11
ABP44688
ID ABP44688 standard; protein; 249 AA.
XX
AC ABP44688;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human BLyS binding scFv SEQ ID 699.
XX
KW BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS Homo sapiens.
XX
PN WO200202641-A1.
XX
PD 10-JAN-2002.
XX
PF 15-JUN-2001; 2001WO-US019110.
XX
PR 16-JUN-2000; 2000US-0212210P.
PR 17-OCT-2000; 2000US-0240816P.
PR 16-MAR-2001; 2001US-0276248P.
PR 21-MAR-2001; 2001US-0277379P.
PR 25-MAY-2001; 2001US-0293499P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX
DR WPI; 2002-114799/15.
XX
PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
PT diagnosis and treatment of cancers and immune disorders.
XX
PS Claim 1; Page 1235-1236; 3148pp; English.
XX
CC This invention describes novel antibodies that immunospecifically bind to
CC B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of BLyS. The antibodies bind to BLyS
CC and so may be used to detect and quantitate the presence of BLyS in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of BLyS. They may also be
CC administered to treat diseases associated with aberrant BLyS expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention
XX
SQ Sequence 249 AA;

Query Match 99.1%; Score 634; DB 5; Length 249;
Best Local Similarity 99.2%; Pred. No. 3.6e-51;
Matches 122; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60

Qy 61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHYGMDVWGRGTMVT 120
|||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db 61 SQNFQGRVAITADESTSTAFMELSSLRSEDTAVYYCARSRDLLLFPHYGMDVWGRGTMVT 120

Qy 121 VSS 123
|||
Db 121 VSS 123

RESULT 12
ABP45737
ID ABP45737 standard; protein; 249 AA.
XX
AC ABP45737;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human BLyS binding scFv SEQ ID 1748.
XX
KW BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS Homo sapiens.
XX

PN WO200202641-A1.
XX
PD 10-JAN-2002.
XX
PF 15-JUN-2001; 2001WO-US019110.
XX
PR 16-JUN-2000; 2000US-0212210P.
PR 17-OCT-2000; 2000US-0240816P.
PR 16-MAR-2001; 2001US-0276248P.
PR 21-MAR-2001; 2001US-0277379P.
PR 25-MAY-2001; 2001US-0293499P.
XX
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PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX
DR WPI; 2002-114799/15.
XX
PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
PT diagnosis and treatment of cancers and immune disorders.
XX
PS Claim 1; Page 2488-2489; 3148pp; English.
XX
CC This invention describes novel antibodies that immunospecifically bind to
CC B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of BLyS. The antibodies bind to BLyS
CC and so may be used to detect and quantitate the presence of BLyS in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of BLyS. They may also be
CC administered to treat diseases associated with aberrant BLyS expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention
XX
SQ Sequence 249 AA;

```
  Query Match             99.1%;  Score 634;  DB 5;  Length 249;
  Best Local Similarity   98.4%;  Pred. No. 3.6e-51;
  Matches  121;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60
              :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60

Qy         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHYGMDVWGRGTMVT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||:||
Db         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHYGMDVWGRGTLVT 120

Qy        121 VSS 123
              |||
Db        121 VSS 123
```

RESULT 13
ABP45297
ID ABP45297 standard; protein; 246 AA.
XX
AC ABP45297;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human BLyS binding scFv SEQ ID 1308.
XX
KW BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS Homo sapiens.
XX
PN WO200202641-A1.
XX
PD 10-JAN-2002.
XX
PF 15-JUN-2001; 2001WO-US019110.
XX
PR 16-JUN-2000; 2000US-0212210P.
PR 17-OCT-2000; 2000US-0240816P.
PR 16-MAR-2001; 2001US-0276248P.
PR 21-MAR-2001; 2001US-0277379P.
PR 25-MAY-2001; 2001US-0293499P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX
DR WPI; 2002-114799/15.
XX
PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
PT diagnosis and treatment of cancers and immune disorders.
XX
PS Claim 1; Page 1964-1965; 3148pp; English.
XX
CC This invention describes novel antibodies that immunospecifically bind to
CC B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of BLyS. The antibodies bind to BLyS
CC and so may be used to detect and quantitate the presence of BLyS in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of BLyS. They may also be
CC administered to treat diseases associated with aberrant BLyS expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention
XX
SQ Sequence 246 AA;

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Qy        121 VSS 123
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Db        121 VSS 123
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ID ABP44677 standard; protein; 249 AA.
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AC ABP44677;

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DT   19-AUG-2002  (first entry)
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DE   Human BLyS binding scFv SEQ ID 688.
XX
KW   BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW   tumour necrosis factor; B cell proliferation; B cell differentiation;
KW   immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW   antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW   systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW   common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS   Homo sapiens.
XX
PN   WO200202641-A1.
XX
PD   10-JAN-2002.
XX
PF   15-JUN-2001; 2001WO-US019110.
XX
PR   16-JUN-2000; 2000US-0212210P.
PR   17-OCT-2000; 2000US-0240816P.
PR   16-MAR-2001; 2001US-0276248P.
PR   21-MAR-2001; 2001US-0277379P.
PR   25-MAY-2001; 2001US-0293499P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
PA   (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI   Ruben SM,  Barash SC,  Choi GH,  Vaughan T,  Hilbert D;
XX
DR   WPI; 2002-114799/15.
XX
PT   Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
PT   diagnosis and treatment of cancers and immune disorders.
XX
PS   Claim 1; Page 1222-1223; 3148pp; English.
XX
CC   This invention describes novel antibodies that immunospecifically bind to
CC   B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the
CC   tumour necrosis factor (TNF) super family and induces B cell
CC   proliferation and differentiation. The antibodies of the invention have
CC   cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC   antirheumatic and antiAIDS activity and can be used in vaccines to
CC   inhibit the expression and activity of BLyS. The antibodies bind to BLyS
CC   and so may be used to detect and quantitate the presence of BLyS in
CC   biological samples and may be used in this way to diagnose disease
CC   associated with aberrant expression of BLyS. They may also be
CC   administered to treat diseases associated with aberrant BLyS expression
CC   and activity such as cancer, immune, and autoimmune disorders and
CC   diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC   immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC   acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC   the antibodies and fragments of the antibodies described in the method of
CC   the invention
XX
SQ   Sequence 249 AA;

  Query Match             98.8%;  Score 632;  DB 5;  Length 249;
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  Matches  122;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Qy         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHYGMDVWGRGTMVT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHYGMDVWGRGTMVT 120

Qy        121 VSS 123
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Db        121 VSS 123
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RESULT 15
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ID   ABP44313 standard; protein; 249 AA.
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AC   ABP44313;
XX
DT   19-AUG-2002  (first entry)
XX
DE   Human BLyS binding scFv SEQ ID 324.
XX
KW   BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW   tumour necrosis factor; B cell proliferation; B cell differentiation;
KW   immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW   antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW   systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW   common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS   Homo sapiens.
XX
PN   WO200202641-A1.
XX
PD   10-JAN-2002.
XX
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PR   16-JUN-2000; 2000US-0212210P.
PR   17-OCT-2000; 2000US-0240816P.
PR   16-MAR-2001; 2001US-0276248P.
PR   21-MAR-2001; 2001US-0277379P.
PR   25-MAY-2001; 2001US-0293499P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
PA   (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI   Ruben SM,  Barash SC,  Choi GH,  Vaughan T,  Hilbert D;
XX
DR   WPI; 2002-114799/15.
XX
PT   Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
PT   diagnosis and treatment of cancers and immune disorders.
XX
PS   Claim 1; Page 790-791; 3148pp; English.
XX
CC   This invention describes novel antibodies that immunospecifically bind to
CC   B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the
CC   tumour necrosis factor (TNF) super family and induces B cell
CC   proliferation and differentiation. The antibodies of the invention have
CC   cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC   antirheumatic and antiAIDS activity and can be used in vaccines to
CC   inhibit the expression and activity of BLyS. The antibodies bind to BLyS
CC   and so may be used to detect and quantitate the presence of BLyS in
CC   biological samples and may be used in this way to diagnose disease
CC   associated with aberrant expression of BLyS. They may also be
CC   administered to treat diseases associated with aberrant BLyS expression
CC   and activity such as cancer, immune, and autoimmune disorders and
CC   diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC   immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC   acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC   the antibodies and fragments of the antibodies described in the method of
CC   the invention
XX
SQ   Sequence 249 AA;

  Query Match             98.8%;  Score 632;  DB 5;  Length 249;
  Best Local Similarity   98.4%;  Pred. No. 5.5e-51;
  Matches  121;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60
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Db          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60
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Qy         121 VSS 123
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Db         121 VSS 123
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Job time : 54.0897 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: September 9, 2004, 11:04:55 ; Search time 15.7692 Seconds
(without alignments)
402.683 Million cell updates/sec

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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 70 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	502	78.4	123	2	US-08-652-816A-8	Sequence 8, Appli
2	501	78.3	123	2	US-08-652-816A-1	Sequence 1, Appli
3	499	78.0	123	2	US-08-652-816A-9	Sequence 9, Appli
4	496	77.5	119	4	US-09-025-769B-21	Sequence 21, Appl
5	494	77.2	123	2	US-08-652-816A-6	Sequence 6, Appli
6	491.5	76.8	120	4	US-09-025-769B-35	Sequence 35, Appl
7	491.5	76.8	120	4	US-09-025-769B-57	Sequence 57, Appl
8	483	75.5	123	2	US-08-652-816A-7	Sequence 7, Appli
9	469	73.3	476	2	US-08-378-939-10	Sequence 10, Appl
10	465.5	72.7	147	1	US-08-217-918-4	Sequence 4, Appli
11	462	72.2	120	2	US-08-428-197-12	Sequence 12, Appl
12	462	72.2	120	5	PCT-US93-10555-12	Sequence 12, Appl
13	458	71.6	121	2	US-08-232-081B-41	Sequence 41, Appl
14	456	71.2	120	2	US-08-428-197-13	Sequence 13, Appl
15	456	71.2	120	5	PCT-US93-10555-13	Sequence 13, Appl
16	453	70.8	119	3	US-08-983-607-50	Sequence 50, Appl
17	432	67.5	122	5	PCT-US95-00067-2	Sequence 2, Appli
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52	427	66.7	117	2	US-08-646-360-166	Sequence 166, App
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59	427	66.7	117	3	US-08-484-537-104	Sequence 104, App
60	427	66.7	117	4	US-09-450-520A-13	Sequence 13, Appl
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62	427	66.7	117	4	US-09-711-485-166	Sequence 166, App
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66	426	66.6	129	2	US-08-561-521-45	Sequence 45, Appl
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68	426	66.6	129	5	PCT-US95-01219-45	Sequence 45, Appl
69	423	66.1	125	3	US-09-199-149-3	Sequence 3, Appli
70	422.5	66.0	139	4	US-09-355-925-8	Sequence 8, Appli

ALIGNMENTS

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RESULT 1
US-08-652-816A-8
; Sequence 8, Application US/08652816A
; Patent No. 5872215
;  GENERAL INFORMATION:
;    APPLICANT:  Osbourn, JK
;    APPLICANT:  Allen, DJ
;    APPLICANT:  McCafferty, JG
;    TITLE OF INVENTION:  Specific binding members, materials and
;    TITLE OF INVENTION:  methods.
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States of America
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/652,816A
;      FILING DATE:  23-MAY-1996
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;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9125579.4
;      FILING DATE:  02-DEC-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9125579.8
;      FILING DATE:  02-DEC-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9206318.9
;      FILING DATE:  24-MAR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9206372.6
;      FILING DATE:  23-SEP-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9525004.9
;      FILING DATE:  07-DEC-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9610824.6
;      FILING DATE:  23-MAY-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/GB92/02240
;      FILING DATE:  02-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/244,597
;      FILING DATE:  01-JUN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  David W. Clough
;      REGISTRATION NUMBER:  36,107
;      REFERENCE/DOCKET NUMBER:  28111/33308
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-474-6300
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  123 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-08-652-816A-8

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  Best Local Similarity   79.7%;  Pred. No. 1.8e-44;
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Qy         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHYGMDVWGRGTMVT 120
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Qy        121 VSS 123
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Db        121 VSS 123


RESULT 2
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; Sequence 1, Application US/08652816A
; Patent No. 5872215
;  GENERAL INFORMATION:
;    APPLICANT:  Osbourn, JK
;    APPLICANT:  Allen, DJ
;    APPLICANT:  McCafferty, JG
;    TITLE OF INVENTION:  Specific binding members, materials and
;    TITLE OF INVENTION:  methods.
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States of America
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/652,816A
;      FILING DATE:  23-MAY-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9125579.4
;      FILING DATE:  02-DEC-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9125579.8
;      FILING DATE:  02-DEC-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9206318.9
;      FILING DATE:  24-MAR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9206372.6
;      FILING DATE:  23-SEP-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9525004.9
;      FILING DATE:  07-DEC-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9610824.6
;      FILING DATE:  23-MAY-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/GB92/02240
;      FILING DATE:  02-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/244,597
;      FILING DATE:  01-JUN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  David W. Clough
;      REGISTRATION NUMBER:  36,107
;      REFERENCE/DOCKET NUMBER:  28111/33308
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-474-6300
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  123 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-08-652-816A-1

  Query Match             78.3%;  Score 501;  DB 2;  Length 123;
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  Matches  100;  Conservative   10;  Mismatches   12;  Indels    2;  Gaps    2;

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RESULT 3
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; Sequence 9, Application US/08652816A
; Patent No. 5872215
;  GENERAL INFORMATION:
;    APPLICANT:  Osbourn, JK
;    APPLICANT:  Allen, DJ
;    APPLICANT:  McCafferty, JG
;    TITLE OF INVENTION:  Specific binding members, materials and
;    TITLE OF INVENTION:  methods.
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
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;       STREET:  6300 Sears Tower, 233 South Wacker Drive
;       CITY:  Chicago
;       STATE:  Illinois
;       COUNTRY:  United States of America
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/652,816A
;       FILING DATE:  23-MAY-1996
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  GB 9125579.4
;       FILING DATE:  02-DEC-1991
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  GB 9125579.8
;       FILING DATE:  02-DEC-1991
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  GB 9206318.9
;       FILING DATE:  24-MAR-1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  GB 9206372.6
;       FILING DATE:  23-SEP-1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  GB 9525004.9
;       FILING DATE:  07-DEC-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  GB 9610824.6
;       FILING DATE:  23-MAY-1996
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/GB92/02240
;       FILING DATE:  02-DEC-1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/244,597
;       FILING DATE:  01-JUN-1994
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  David W. Clough
;       REGISTRATION NUMBER:  36,107
;       REFERENCE/DOCKET NUMBER:  28111/33308
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  312-474-6300
;   INFORMATION FOR SEQ ID NO:  9:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  123 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
US-08-652-816A-9

  Query Match             78.0%;  Score 499;  DB 2;  Length 123;
  Best Local Similarity   80.6%;  Pred. No. 3.7e-44;
  Matches  100;  Conservative    9;  Mismatches   13;  Indels    2;  Gaps    2;

Qy          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60
              |||| |||||||||||||:|||||||||:|: |||:|||||||||||| ||| |||| |
Db          1 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSNSPINWLRQAPGQGLEWMGSIIPSFGTANY 60

Qy         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCA-RSRDLLLFPHYGMDVWGRGTMV 119
              :| ||||: |||||||||| |||||||||||||||| ||    |: :| |||||:|||| 
Db         61 AQKFQGRLTITADESTSTAYMELSSLRSEDTAVYYCAGRSHTYELY-YYYMDVWGQGTMV 119

Qy        120 TVSS 123
              ||||
Db        120 TVSS 123


RESULT 4
US-09-025-769B-21
; Sequence 21, Application US/09025769B
; Patent No. 6300064
;  GENERAL INFORMATION:
;    APPLICANT:  Knappik, Achim
;    APPLICANT:  Pack, Peter
;    APPLICANT:  Ilag, Vic
;    APPLICANT:  Ge, Liming
;    APPLICANT:  Moroney, Simon
;    APPLICANT:  Plueckthun, Andreas
;    TITLE OF INVENTION:  Protein/(Poly)peptide libraries
;    NUMBER OF SEQUENCES:  373
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  James F. Haley, Jr., Esq. c/o Fish & Neave
;      STREET:  1251 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10021
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/025,769B
;      FILING DATE:  18-FEB-1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 95 11 3021.0
;      FILING DATE:  18-AUG-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  James F. Haley, Jr., Esq.
;      REGISTRATION NUMBER:  27,794
;      REFERENCE/DOCKET NUMBER:  MORPHO/5
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212)596-9000
;      TELEFAX:  (212)596-9090
;  INFORMATION FOR SEQ ID NO:  21:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-025-769B-21

  Query Match             77.5%;  Score 496;  DB 4;  Length 119;
  Best Local Similarity   79.2%;  Pred. No. 7.2e-44;
  Matches   99;  Conservative    9;  Mismatches    9;  Indels    8;  Gaps    2;

Qy          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60
              |||| |||||||||||||:|||||||||:: ||:|||||||||||||||||:|||| |
Db          1 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY 60

Qy         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHY--GMDVWGRGTM 118
              :| ||||| |||||||||| ||||||||||||||||:      | |  | | ||:||:
Db         61 AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARA------PGYCSGFDYWGQGTL 114

Qy        119 VTVSS 123
              |||||
Db        115 VTVSS 119


RESULT 5
US-08-652-816A-6
; Sequence 6, Application US/08652816A
; Patent No. 5872215
;  GENERAL INFORMATION:
;    APPLICANT:  Osbourn, JK
;    APPLICANT:  Allen, DJ
;    APPLICANT:  McCafferty, JG
;    TITLE OF INVENTION:  Specific binding members, materials and
;    TITLE OF INVENTION:  methods.
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
```

```
;       COUNTRY:  United States of America
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/652,816A
;       FILING DATE:  23-MAY-1996
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  GB 9125579.4
;       FILING DATE:  02-DEC-1991
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  GB 9125579.8
;       FILING DATE:  02-DEC-1991
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  GB 9206318.9
;       FILING DATE:  24-MAR-1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  GB 9206372.6
;       FILING DATE:  23-SEP-1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  GB 9525004.9
;       FILING DATE:  07-DEC-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  GB 9610824.6
;       FILING DATE:  23-MAY-1996
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/GB92/02240
;       FILING DATE:  02-DEC-1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/244,597
;       FILING DATE:  01-JUN-1994
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  David W. Clough
;       REGISTRATION NUMBER:  36,107
;       REFERENCE/DOCKET NUMBER:  28111/33308
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  312-474-6300
;   INFORMATION FOR SEQ ID NO:  6:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  123 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
US-08-652-816A-6

  Query Match             77.2%;  Score 494;  DB 2;  Length 123;
  Best Local Similarity   78.9%;  Pred. No. 1.2e-43;
  Matches   97;  Conservative    8;  Mismatches   18;  Indels    0;  Gaps    0;

Qy          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60
              |||| |||||||||||||:||||||||||:|: |||:|||||||||||| ||| |||| |
Db          1 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSNSPINWLRQAPGQGLEWMGSIIPSFGTANY 60

Qy         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHYGMDVWGRGTMVT 120
              :| ||||: |||||||||| |||||||||||||||         :| |||||:|||||
Db         61 AQKFQGRLTITADESTSTAYMELSSLRSEDTAVYYCAGCSHNYELYYYYMDVWGQGTMVT 120

Qy        121 VSS 123
              |||
Db        121 VSS 123


RESULT 6
US-09-025-769B-35
; Sequence 35, Application US/09025769B
; Patent No. 6300064
;  GENERAL INFORMATION:
;    APPLICANT:  Knappik, Achim
;    APPLICANT:  Pack, Peter
;    APPLICANT:  Ilag, Vic
;    APPLICANT:  Ge, Liming
;    APPLICANT:  Moroney, Simon
;    APPLICANT:  Plueckthun, Andreas
;    TITLE OF INVENTION:  Protein/(Poly)peptide libraries
;    NUMBER OF SEQUENCES:  373
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  James F. Haley, Jr., Esq. c/o Fish & Neave
;      STREET:  1251 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10021
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/025,769B
;      FILING DATE:  18-FEB-1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 95 11 3021.0
;      FILING DATE:  18-AUG-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  James F. Haley, Jr., Esq.
;      REGISTRATION NUMBER:  27,794
;      REFERENCE/DOCKET NUMBER:  MORPHO/5
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212)596-9000
;      TELEFAX:  (212)596-9090
;  INFORMATION FOR SEQ ID NO:  35:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  120 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-025-769B-35

  Query Match             76.8%;  Score 491.5;  DB 4;  Length 120;
  Best Local Similarity   79.8%;  Pred. No. 2.1e-43;
  Matches   99;  Conservative    8;  Mismatches   12;  Indels    5;  Gaps    2;

Qy          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60
              |||| |||||||||||||:||||||||||:: ||:|||||||||||||||||:|||| |
Db          1 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY 60

Qy         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCAR-SRDLLLFPHYGMDVWGRGTMV 119
              :| ||||| |||||||||| |||||||||||||||||   |      | || ||:||:|
Db         61 AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARWGGD----GFYAMDYWGQGTLV 116

Qy        120 TVSS 123
              ||||
Db        117 TVSS 120


RESULT 7
US-09-025-769B-57
; Sequence 57, Application US/09025769B
; Patent No. 6300064
;  GENERAL INFORMATION:
;    APPLICANT:  Knappik, Achim
;    APPLICANT:  Pack, Peter
;    APPLICANT:  Ilag, Vic
;    APPLICANT:  Ge, Liming
;    APPLICANT:  Moroney, Simon
;    APPLICANT:  Plueckthun, Andreas
;    TITLE OF INVENTION:  Protein/(Poly)peptide libraries
;    NUMBER OF SEQUENCES:  373
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  James F. Haley, Jr., Esq. c/o Fish & Neave
;      STREET:  1251 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
```

```
;       ZIP:  10021
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30 (EPO)
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/025,769B
;       FILING DATE:  18-FEB-1998
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  EP 95 11 3021.0
;       FILING DATE:  18-AUG-1995
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  James F. Haley, Jr., Esq.
;       REGISTRATION NUMBER:  27,794
;       REFERENCE/DOCKET NUMBER:  MORPHO/5
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (212)596-9000
;       TELEFAX:  (212)596-9090
;   INFORMATION FOR SEQ ID NO:  57:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  120 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-09-025-769B-57

  Query Match             76.8%;  Score 491.5;  DB 4;  Length 120;
  Best Local Similarity   79.8%;  Pred. No. 2.1e-43;
  Matches   99;  Conservative    8;  Mismatches   12;  Indels    5;  Gaps    2;

Qy          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60
              |||| |||||||||||||:|||||||||:: ||:||||||||||||||||:|||| |
Db          1 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY 60

Qy         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCAR-SRDLLLFPHYGMDVWGRGTMV 119
              :| ||||| |||||||||| ||||||||||||||||||    |      | || ||:||:|
Db         61 AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARWGGD----GFYAMDYWGQGTLV 116

Qy        120 TVSS 123
              ||||
Db        117 TVSS 120


RESULT 8
US-08-652-816A-7
; Sequence 7, Application US/08652816A
; Patent No. 5872215
;  GENERAL INFORMATION:
;    APPLICANT:  Osbourn, JK
;    APPLICANT:  Allen, DJ
;    APPLICANT:  McCafferty, JG
;    TITLE OF INVENTION:  Specific binding members, materials and
;    TITLE OF INVENTION:  methods.
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States of America
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/652,816A
;      FILING DATE:  23-MAY-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9125579.4
;      FILING DATE:  02-DEC-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9125579.8
;      FILING DATE:  02-DEC-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9206318.9
;      FILING DATE:  24-MAR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9206372.6
;      FILING DATE:  23-SEP-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9525004.9
;      FILING DATE:  07-DEC-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9610824.6
;      FILING DATE:  23-MAY-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/GB92/02240
;      FILING DATE:  02-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/244,597
;      FILING DATE:  01-JUN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  David W. Clough
;      REGISTRATION NUMBER:  36,107
;      REFERENCE/DOCKET NUMBER:  28111/33308
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-474-6300
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  123 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-08-652-816A-7

  Query Match             75.5%;  Score 483;  DB 2;  Length 123;
  Best Local Similarity   78.0%;  Pred. No. 1.6e-42;
  Matches   96;  Conservative    9;  Mismatches   18;  Indels    0;  Gaps    0;

Qy          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60
              |||| |||||||||||||:|||||||||:|: |||:|||||||||||| ||| |||| |
Db          1 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSNSPINWLRQAPGQGLEWMGSIIPSFGTANY 60

Qy         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHYGMDVWGRGTMVT 120
              :| ||||: |||||||||| |||||||||||||||| :       :| ||| |:|||||
Db         61 AQKFQGRLTITADESTSTAYMELSSLRSEDTAVYYCAGANSCNRSYYYYMDVRGQGTMVT 120

Qy        121 VSS 123
              |||
Db        121 VSS 123


RESULT 9
US-08-378-939-10
; Sequence 10, Application US/08378939
; Patent No. 5876961
;  GENERAL INFORMATION:
;    APPLICANT:  CROWE, JAMES SCOTT
;    APPLICANT:  LEWIS, ALAN PETER
;    TITLE OF INVENTION:  PRODUCTION OF ANTIBODIES
;    NUMBER OF SEQUENCES:  46
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ROTHWELL, FIGG, ERNST & KURZ
;      STREET:  555 THIRTEENTH ST. N.W.
;      CITY:  WASHINGTON
;      STATE:  D. C.
;      COUNTRY:  U.S.
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/378,939
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;       FILING DATE:
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/952640
;       FILING DATE:  01-DEC-1992
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  ERNST, BARBARA G
;       REGISTRATION NUMBER:  30,377
;       REFERENCE/DOCKET NUMBER:  1808-118
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (202) 783-6040
;       TELEFAX:  (202) 783-6031
;   INFORMATION FOR SEQ ID NO:  10:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  476 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-378-939-10

  Query Match             73.3%;  Score 469;  DB 2;  Length 476;
  Best Local Similarity   70.9%;  Pred. No. 2.2e-40;
  Matches   95;  Conservative    9;  Mismatches   12;  Indels   18;  Gaps    2;

Qy          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60
              |:|: |||||||||||| |||||||||:| ||:||||||||||||||||:|||  |
Db         20 QMQVVQSGAEVKKPGSSVTVSCKASGGTFSNYAISWVRQAPGQGLEWMGGIIPLFGTPTY 79

Qy         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHY----------G 109
              |||||||| ||||:||||| |||:|||||||||||||  |       |
Db         80 SQNFQGRVTITADKSTSTAHMELTSLRSEDTAVYYCATDR-------YRQANFDRARVGW 132

Qy        110 MDVWGRGTMVTVSS 123
               | ||:||:|||||
Db        133 FDPWGQGTLVTVSS 146


RESULT 10
US-08-217-918-4
; Sequence 4, Application US/08217918
; Patent No. 5506132
;  GENERAL INFORMATION:
;    APPLICANT:  LAKE, PHILIP
;    APPLICANT:  OSTBERG, LARS
;    TITLE OF INVENTION:  HUMAN ANTIBODIES AGAINST
;    TITLE OF INVENTION:  VARICELLA-ZOSTER VIRUS
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  379 Lytton Avenue
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94301
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/217,918
;      FILING DATE:  24-MAR-1994
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, Willaim M
;      REGISTRATION NUMBER:  30,223
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  147 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-217-918-4

  Query Match             72.7%;  Score 465.5;  DB 1;  Length 147;
  Best Local Similarity   71.8%;  Pred. No. 1.3e-40;
  Matches   94;  Conservative   12;  Mismatches   14;  Indels   11;  Gaps    2;

Qy          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60
              |||| |||||||||||||:|||||||||:| ||:|||||||||||||| |:|:| |: |
Db         20 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSNFAISWVRQAPGQGLEWMGRIMPLFVTSTY 79

Qy         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFP--------HYGMDV 112
              :| ||||| |:|| ||||| ||||||||:|||:|||||    :  |         |||||
Db         80 AQKFQGRVTISADASTSTAYMELSSLRSDDTAMYYCARD---ITAPGAAPTPLNFYGMDV 136

Qy        113 WGRGTMVTVSS 123
              ||:|| |||||
Db        137 WGQGTTVTVSS 147


RESULT 11
US-08-428-197-12
; Sequence 12, Application US/08428197
; Patent No. 5891438
;  GENERAL INFORMATION:
;    APPLICANT:  SILVERMAN, GREGG J.
;    TITLE OF INVENTION:  METHOD FOR STIMULATING PRODUCTION OF
;    TITLE OF INVENTION:  VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH
;    TITLE OF INVENTION:  VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES
;    TITLE OF INVENTION:  THEREOF
;    NUMBER OF SEQUENCES:  51
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Spensley Horn Jubas & Lubitz
;      STREET:  1880 Century Park East - Suite 500
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  90067
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/428,197
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/10555
;      FILING DATE:  29-OCT-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Howells, Stacy L.
;      REGISTRATION NUMBER:  34,842
;      REFERENCE/DOCKET NUMBER:  FD-2630
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 455-5100
;      TELEFAX:  (619) 455-5110
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  120 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    IMMEDIATE SOURCE:
;      CLONE:  BOR
;    FEATURE:
;      NAME/KEY:  Peptide
;      LOCATION:  1..120
US-08-428-197-12

  Query Match             72.2%;  Score 462;  DB 2;  Length 120;
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  Best Local Similarity   74.0%;  Pred. No. 2.3e-40;
  Matches   91;  Conservative   14;  Mismatches   14;  Indels    4;  Gaps    2;

Qy          2 VQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKYS 61
              ||| |||||||||||||:|:||||| ||:::||:||||||||||||||||:|||  |:
Db          1 VQLVQSGAEVKKPGSSVKVTCKASGDTFSSSAISWVRQAPGQGLEWMGGIIPIFGTPNYA 60

Qy         62 QNFQGRVAITADESTSTASMELSSLRSEDTAVYYCAR-SRDLLLFPHYGMDVWGRGTMVT 120
              | ||||| || ||||||| ||:||||||||:|||||  | : : |    | ||:||:||
Db         61 QKFQGRVTITTDESTSTAYMEVSSLRSEDTALYYCAREGRRMAINP---FDYWGQGTLVT 117

Qy        121 VSS 123
              |||
Db        118 VSS 120


RESULT 12
PCT-US93-10555-12
; Sequence 12, Application PC/TUS9310555
;  GENERAL INFORMATION:
;    APPLICANT:  SILVERMAN, GREGG J.
;    TITLE OF INVENTION:  METHOD FOR STIMULATING PRODUCTION OF
;    TITLE OF INVENTION:  VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH
;    TITLE OF INVENTION:  VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES
;    TITLE OF INVENTION:  THEREOF
;    NUMBER OF SEQUENCES:  51
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Spensley Horn Jubas & Lubitz
;      STREET:  1880 Century Park East - Suite 500
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  90067
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/10555
;      FILING DATE:  29-OCT-1993
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Howells, Stacy L.
;      REGISTRATION NUMBER:  34,842
;      REFERENCE/DOCKET NUMBER:  FD-2630
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 455-5100
;      TELEFAX:  (619) 455-5110
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  120 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    IMMEDIATE SOURCE:
;      CLONE:  BOR
;    FEATURE:
;      NAME/KEY:  Peptide
;      LOCATION:  1..120
PCT-US93-10555-12

  Query Match             72.2%;  Score 462;  DB 5;  Length 120;
  Best Local Similarity   74.0%;  Pred. No. 2.3e-40;
  Matches   91;  Conservative   14;  Mismatches   14;  Indels    4;  Gaps    2;

Qy          2 VQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKYS 61
              ||| |||||||||||||:|:||||| ||:::||:||||||||||||||||:|||  |:
Db          1 VQLVQSGAEVKKPGSSVKVTCKASGDTFSSSAISWVRQAPGQGLEWMGGIIPIFGTPNYA 60

Qy         62 QNFQGRVAITADESTSTASMELSSLRSEDTAVYYCAR-SRDLLLFPHYGMDVWGRGTMVT 120
              | ||||| || ||||||| ||:||||||||:|||||  | : : |    | ||:||:||
Db         61 QKFQGRVTITTDESTSTAYMEVSSLRSEDTALYYCAREGRRMAINP---FDYWGQGTLVT 117

Qy        121 VSS 123
              |||
Db        118 VSS 120


RESULT 13
US-08-232-081B-41
; Sequence 41, Application US/08232081B
; Patent No. 5886152
;  GENERAL INFORMATION:
;    APPLICANT:  NAKATANI, TOMOYUKI
;    APPLICANT:  GOMI, HIDEYUKI
;    APPLICANT:  WIJDENES, JOHN
;    APPLICANT:  NOGUCHI, HIROSHI
;    TITLE OF INVENTION:  HUMANIZED B-B10
;    NUMBER OF SEQUENCES:  42
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BIRCH, STEWART, KOLASCH AND BIRCH
;      STREET:  PO BOX 747
;      CITY:  FALLS CHURCH
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22040-0747
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/232,081B
;      FILING DATE:
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SVENSSON, LEONARD R
;      REGISTRATION NUMBER:  30,330
;      REFERENCE/DOCKET NUMBER:  20-3484
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 205-8000
;      TELEFAX:  (703) 205-8050
;  INFORMATION FOR SEQ ID NO:  41:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  121 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-232-081B-41

  Query Match             71.6%;  Score 458;  DB 2;  Length 121;
  Best Local Similarity   72.0%;  Pred. No. 6e-40;
  Matches   90;  Conservative   14;  Mismatches   15;  Indels    6;  Gaps    2;

Qy          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60
              :| | |||||||||||||:||||||||:: ||:||||||||||||||||:|| | |
Db          1 EVHLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGQANY 60

Qy         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHYG--MDVWGRGTM 118
              :| ||||| |||||||:|| ||| ||||:|||:||||:      :  ||   | ||:||:
Db         61 AQKFQGRVTITADESTNTAYMELRSLRSDDTAMYYCAKEG----YGDYGRPFDFWGQGTL 116

Qy        119 VTVSS 123
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Db        117 VTVSS 121


RESULT 14
US-08-428-197-13
; Sequence 13, Application US/08428197
; Patent No. 5891438
;  GENERAL INFORMATION:
;    APPLICANT:  SILVERMAN, GREGG J.
```

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;    TITLE OF INVENTION:  METHOD FOR STIMULATING PRODUCTION OF
;    TITLE OF INVENTION:  VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH
;    TITLE OF INVENTION:  VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES
;    TITLE OF INVENTION:  THEREOF
;    NUMBER OF SEQUENCES:  51
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Spensley Horn Jubas & Lubitz
;      STREET:  1880 Century Park East - Suite 500
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  90067
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/428,197
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/10555
;      FILING DATE:  29-OCT-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Howells, Stacy L.
;      REGISTRATION NUMBER:  34,842
;      REFERENCE/DOCKET NUMBER:  FD-2630
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 455-5100
;      TELEFAX:  (619) 455-5110
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  120 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    IMMEDIATE SOURCE:
;      CLONE:  KAS
;    FEATURE:
;      NAME/KEY:  Peptide
;      LOCATION:  1..120
US-08-428-197-13

  Query Match             71.2%;  Score 456;  DB 2;  Length 120;
  Best Local Similarity   72.6%;  Pred. No. 9.6e-40;
  Matches   90;  Conservative   13;  Mismatches   15;  Indels    6;  Gaps    2;

Qy          2 VQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKYS 61
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Db          1 VHLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGQANYA 60

Qy         62 QNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHYG--MDVWGRGTMV 119
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Db         61 QKFQGRVTITADESTNTAYMELRSLRSDDTAMYYCAKEG----YGDYGRPFDFWGQGTLV 116

Qy        120 TVSS 123
              ||||
Db        117 TVSS 120


RESULT 15
PCT-US93-10555-13
; Sequence 13, Application PC/TUS9310555
;  GENERAL INFORMATION:
;    APPLICANT:  SILVERMAN, GREGG J.
;    TITLE OF INVENTION:  METHOD FOR STIMULATING PRODUCTION OF
;    TITLE OF INVENTION:  VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH
;    TITLE OF INVENTION:  VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES
;    TITLE OF INVENTION:  THEREOF
;    NUMBER OF SEQUENCES:  51
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Spensley Horn Jubas & Lubitz
;      STREET:  1880 Century Park East - Suite 500
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  90067
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/10555
;      FILING DATE:  29-OCT-1993
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Howells, Stacy L.
;      REGISTRATION NUMBER:  34,842
;      REFERENCE/DOCKET NUMBER:  FD-2630
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 455-5100
;      TELEFAX:  (619) 455-5110
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  120 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    IMMEDIATE SOURCE:
;      CLONE:  KAS
;    FEATURE:
;      NAME/KEY:  Peptide
;      LOCATION:  1..120
PCT-US93-10555-13

  Query Match             71.2%;  Score 456;  DB 5;  Length 120;
  Best Local Similarity   72.6%;  Pred. No. 9.6e-40;
  Matches   90;  Conservative   13;  Mismatches   15;  Indels    6;  Gaps    2;

Qy          2 VQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKYS 61
              | | ||||||||||||||:||||||||||:: ||:||||||||||||||||||:|| | |:
Db          1 VHLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGQANYA 60

Qy         62 QNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHYG--MDVWGRGTMV 119
              | ||||| ||||||:|| ||| ||||:|||:||||:      :  ||   | ||:||:|
Db         61 QKFQGRVTITADESTNTAYMELRSLRSDDTAMYYCAKEG----YGDYGRPFDFWGQGTLV 116

Qy        120 TVSS 123
              ||||
Db        117 TVSS 120


Search completed: September  9, 2004, 11:09:18
Job time : 16.7692 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: September 9, 2004, 11:07:30 ; Search time 90.4103 Seconds
(without alignments)
436.287 Million cell updates/sec

Title: US-09-880-748-2_COPY_1_123
Perfect score: 640
Sequence: 1 QVQLQQSGAEVKKPGSSVRV.....LFPHYGMDVWGRGTMVTVSS 123

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1335176 seqs, 320689617 residues

Total number of hits satisfying chosen parameters: 1335176

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 70 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
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12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
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15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
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18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	640	100.0	246	10	US-09-880-748-928	Sequence 928, App
2	640	100.0	246	12	US-10-293-418-928	Sequence 928, App
3	640	100.0	249	10	US-09-880-748-2	Sequence 2, Appli
4	640	100.0	249	10	US-09-880-748-471	Sequence 471, App
5	640	100.0	249	10	US-09-880-748-479	Sequence 479, App
6	640	100.0	249	10	US-09-880-748-618	Sequence 618, App
7	640	100.0	249	10	US-09-880-748-719	Sequence 719, App
8	640	100.0	249	10	US-09-880-748-796	Sequence 796, App
9	640	100.0	249	12	US-10-293-418-2	Sequence 2, Appli
10	640	100.0	249	12	US-10-293-418-471	Sequence 471, App
11	640	100.0	249	12	US-10-293-418-479	Sequence 479, App
12	640	100.0	249	12	US-10-293-418-618	Sequence 618, App
13	640	100.0	249	12	US-10-293-418-719	Sequence 719, App
14	640	100.0	249	12	US-10-293-418-796	Sequence 796, App
15	637	99.5	246	10	US-09-880-748-1426	Sequence 1426, Ap
16	637	99.5	246	10	US-09-880-748-1781	Sequence 1781, Ap
17	637	99.5	246	12	US-10-293-418-1426	Sequence 1426, Ap
18	637	99.5	246	12	US-10-293-418-1781	Sequence 1781, Ap
19	637	99.5	249	10	US-09-880-748-613	Sequence 613, App
20	637	99.5	249	12	US-10-293-418-613	Sequence 613, App
21	634	99.1	249	10	US-09-880-748-699	Sequence 699, App
22	634	99.1	249	10	US-09-880-748-1748	Sequence 1748, Ap
23	634	99.1	249	12	US-10-293-418-699	Sequence 699, App
24	634	99.1	249	12	US-10-293-418-1748	Sequence 1748, Ap
25	633	98.9	246	10	US-09-880-748-1308	Sequence 1308, Ap
26	633	98.9	246	12	US-10-293-418-1308	Sequence 1308, Ap
27	632	98.8	249	10	US-09-880-748-324	Sequence 324, App
28	632	98.8	249	10	US-09-880-748-688	Sequence 688, App
29	632	98.8	249	12	US-10-293-418-324	Sequence 324, App
30	632	98.8	249	12	US-10-293-418-688	Sequence 688, App
31	631	98.6	246	10	US-09-880-748-1818	Sequence 1818, Ap
32	631	98.6	246	12	US-10-293-418-1818	Sequence 1818, Ap
33	631	98.6	249	10	US-09-880-748-721	Sequence 721, App
34	631	98.6	249	12	US-10-293-418-721	Sequence 721, App
35	626	97.8	249	10	US-09-880-748-786	Sequence 786, App
36	626	97.8	249	10	US-09-880-748-794	Sequence 794, App
37	626	97.8	249	10	US-09-880-748-804	Sequence 804, App
38	626	97.8	249	12	US-10-293-418-786	Sequence 786, App
39	626	97.8	249	12	US-10-293-418-794	Sequence 794, App
40	626	97.8	249	12	US-10-293-418-804	Sequence 804, App
41	623	97.3	249	10	US-09-880-748-325	Sequence 325, App
42	623	97.3	249	10	US-09-880-748-761	Sequence 761, App
43	623	97.3	249	10	US-09-880-748-815	Sequence 815, App
44	623	97.3	249	12	US-10-293-418-325	Sequence 325, App
45	623	97.3	249	12	US-10-293-418-761	Sequence 761, App
46	623	97.3	249	12	US-10-293-418-815	Sequence 815, App
47	621	97.0	249	10	US-09-880-748-322	Sequence 322, App
48	621	97.0	249	10	US-09-880-748-329	Sequence 329, App
49	621	97.0	249	10	US-09-880-748-461	Sequence 461, App
50	621	97.0	249	10	US-09-880-748-744	Sequence 744, App
51	621	97.0	249	10	US-09-880-748-752	Sequence 752, App
52	621	97.0	249	10	US-09-880-748-774	Sequence 774, App
53	621	97.0	249	10	US-09-880-748-792	Sequence 792, App
54	621	97.0	249	10	US-09-880-748-797	Sequence 797, App
55	621	97.0	249	10	US-09-880-748-808	Sequence 808, App
56	621	97.0	249	10	US-09-880-748-811	Sequence 811, App
57	621	97.0	249	10	US-09-880-748-825	Sequence 825, App
58	621	97.0	249	10	US-09-880-748-826	Sequence 826, App
59	621	97.0	249	12	US-10-293-418-322	Sequence 322, App
60	621	97.0	249	12	US-10-293-418-329	Sequence 329, App
61	621	97.0	249	12	US-10-293-418-461	Sequence 461, App
62	621	97.0	249	12	US-10-293-418-744	Sequence 744, App
63	621	97.0	249	12	US-10-293-418-752	Sequence 752, App
64	621	97.0	249	12	US-10-293-418-774	Sequence 774, App
65	621	97.0	249	12	US-10-293-418-792	Sequence 792, App
66	621	97.0	249	12	US-10-293-418-797	Sequence 797, App
67	621	97.0	249	12	US-10-293-418-808	Sequence 808, App
68	621	97.0	249	12	US-10-293-418-811	Sequence 811, App
69	621	97.0	249	12	US-10-293-418-825	Sequence 825, App
70	621	97.0	249	12	US-10-293-418-826	Sequence 826, App

ALIGNMENTS

RESULT 1
US-09-880-748-928
; Sequence 928, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816

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;  PRIOR FILING DATE: 2000-10-17
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  NUMBER OF SEQ ID NOS: 3239
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 928
;   LENGTH: 246
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-880-748-928

  Query Match             100.0%;  Score 640;  DB 10;  Length 246;
  Best Local Similarity   100.0%;  Pred. No. 8.7e-57;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60
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Db          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60

Qy         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHYGMDVWGRGTMVT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHYGMDVWGRGTMVT 120

Qy        121 VSS 123
              |||
Db        121 VSS 123


RESULT 2
US-10-293-418-928
; Sequence 928, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523P2
;  CURRENT APPLICATION NUMBER: US/10/293,418
;  CURRENT FILING DATE:  2002-11-27
;  PRIOR APPLICATION NUMBER: 60/331,469
;  PRIOR FILING DATE: 2001-11-16
;  PRIOR APPLICATION NUMBER: 60/340,817
;  PRIOR FILING DATE: 2001-12-19
;  PRIOR APPLICATION NUMBER: 09/880,748
;  PRIOR FILING DATE: 2001-06-15
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  PRIOR APPLICATION NUMBER: 60/212,210
;  PRIOR FILING DATE: 2000-06-16
;  NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 928
;   LENGTH: 246
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-293-418-928

  Query Match             100.0%;  Score 640;  DB 12;  Length 246;
  Best Local Similarity   100.0%;  Pred. No. 8.7e-57;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60

Qy         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHYGMDVWGRGTMVT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHYGMDVWGRGTMVT 120

Qy        121 VSS 123
              |||
Db        121 VSS 123


RESULT 3
US-09-880-748-2
; Sequence 2, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523
;  CURRENT APPLICATION NUMBER: US/09/880,748
;  CURRENT FILING DATE:  2001-06-15
;  PRIOR APPLICATION NUMBER: 60/212,210
;  PRIOR FILING DATE: 2000-06-15
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  NUMBER OF SEQ ID NOS: 3239
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 249
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-880-748-2

  Query Match             100.0%;  Score 640;  DB 10;  Length 249;
  Best Local Similarity   100.0%;  Pred. No. 8.8e-57;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60

Qy         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHYGMDVWGRGTMVT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHYGMDVWGRGTMVT 120

Qy        121 VSS 123
              |||
Db        121 VSS 123


RESULT 4
US-09-880-748-471
; Sequence 471, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523
;  CURRENT APPLICATION NUMBER: US/09/880,748
;  CURRENT FILING DATE:  2001-06-15
;  PRIOR APPLICATION NUMBER: 60/212,210
;  PRIOR FILING DATE: 2000-06-15
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/293,499
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;  PRIOR FILING DATE: 2001-05-25
;  NUMBER OF SEQ ID NOS: 3239
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 471
;   LENGTH: 249
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-880-748-471

  Query Match           100.0%;  Score 640;  DB 10;  Length 249;
  Best Local Similarity  100.0%;  Pred. No. 8.8e-57;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60

Qy         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHYGMDVWGRGTMVT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHYGMDVWGRGTMVT 120

Qy        121 VSS 123
              |||
Db        121 VSS 123


RESULT 5
US-09-880-748-479
; Sequence 479, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523
;  CURRENT APPLICATION NUMBER: US/09/880,748
;  CURRENT FILING DATE:  2001-06-15
;  PRIOR APPLICATION NUMBER: 60/212,210
;  PRIOR FILING DATE: 2000-06-15
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  NUMBER OF SEQ ID NOS: 3239
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 479
;   LENGTH: 249
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-880-748-479

  Query Match           100.0%;  Score 640;  DB 10;  Length 249;
  Best Local Similarity  100.0%;  Pred. No. 8.8e-57;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60

Qy         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHYGMDVWGRGTMVT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHYGMDVWGRGTMVT 120

Qy        121 VSS 123
              |||
Db        121 VSS 123


RESULT 6
US-09-880-748-618
; Sequence 618, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523
;  CURRENT APPLICATION NUMBER: US/09/880,748
;  CURRENT FILING DATE:  2001-06-15
;  PRIOR APPLICATION NUMBER: 60/212,210
;  PRIOR FILING DATE: 2000-06-15
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  NUMBER OF SEQ ID NOS: 3239
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 618
;   LENGTH: 249
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-880-748-618

  Query Match           100.0%;  Score 640;  DB 10;  Length 249;
  Best Local Similarity  100.0%;  Pred. No. 8.8e-57;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60

Qy         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHYGMDVWGRGTMVT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHYGMDVWGRGTMVT 120

Qy        121 VSS 123
              |||
Db        121 VSS 123


RESULT 7
US-09-880-748-719
; Sequence 719, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523
;  CURRENT APPLICATION NUMBER: US/09/880,748
;  CURRENT FILING DATE:  2001-06-15
;  PRIOR APPLICATION NUMBER: 60/212,210
;  PRIOR FILING DATE: 2000-06-15
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  NUMBER OF SEQ ID NOS: 3239
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 719
;   LENGTH: 249
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-880-748-719

  Query Match           100.0%;  Score 640;  DB 10;  Length 249;
  Best Local Similarity  100.0%;  Pred. No. 8.8e-57;
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  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60

Qy         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHYGMDVWGRGTMVT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHYGMDVWGRGTMVT 120

Qy        121 VSS 123
              |||
Db        121 VSS 123


RESULT 8
US-09-880-748-796
; Sequence 796, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523
;  CURRENT APPLICATION NUMBER: US/09/880,748
;  CURRENT FILING DATE:  2001-06-15
;  PRIOR APPLICATION NUMBER: 60/212,210
;  PRIOR FILING DATE: 2000-06-15
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  NUMBER OF SEQ ID NOS: 3239
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 796
;   LENGTH: 249
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-880-748-796

  Query Match             100.0%;  Score 640;  DB 10;  Length 249;
  Best Local Similarity   100.0%;  Pred. No. 8.8e-57;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60

Qy         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHYGMDVWGRGTMVT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHYGMDVWGRGTMVT 120

Qy        121 VSS 123
              |||
Db        121 VSS 123


RESULT 9
US-10-293-418-2
; Sequence 2, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523P2
;  CURRENT APPLICATION NUMBER: US/10/293,418
;  CURRENT FILING DATE:  2002-11-27
;  PRIOR APPLICATION NUMBER: 60/331,469
;  PRIOR FILING DATE: 2001-11-16
;  PRIOR APPLICATION NUMBER: 60/340,817
;  PRIOR FILING DATE: 2001-12-19
;  PRIOR APPLICATION NUMBER: 09/880,748
;  PRIOR FILING DATE: 2001-06-15
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  PRIOR APPLICATION NUMBER: 60/212,210
;  PRIOR FILING DATE: 2000-06-16
;  NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2
;   LENGTH: 249
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-293-418-2

  Query Match             100.0%;  Score 640;  DB 12;  Length 249;
  Best Local Similarity   100.0%;  Pred. No. 8.8e-57;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60

Qy         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHYGMDVWGRGTMVT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHYGMDVWGRGTMVT 120

Qy        121 VSS 123
              |||
Db        121 VSS 123


RESULT 10
US-10-293-418-471
; Sequence 471, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523P2
;  CURRENT APPLICATION NUMBER: US/10/293,418
;  CURRENT FILING DATE:  2002-11-27
;  PRIOR APPLICATION NUMBER: 60/331,469
;  PRIOR FILING DATE: 2001-11-16
;  PRIOR APPLICATION NUMBER: 60/340,817
;  PRIOR FILING DATE: 2001-12-19
;  PRIOR APPLICATION NUMBER: 09/880,748
;  PRIOR FILING DATE: 2001-06-15
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  PRIOR APPLICATION NUMBER: 60/212,210
;  PRIOR FILING DATE: 2000-06-16
;  NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 471
;   LENGTH: 249
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-293-418-471

  Query Match             100.0%;  Score 640;  DB 12;  Length 249;
  Best Local Similarity   100.0%;  Pred. No. 8.8e-57;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60

Qy         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHYGMDVWGRGTMVT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHYGMDVWGRGTMVT 120

Qy        121 VSS 123
              |||
Db        121 VSS 123


RESULT 11
US-10-293-418-479
; Sequence 479, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523P2
;  CURRENT APPLICATION NUMBER: US/10/293,418
;  CURRENT FILING DATE:  2002-11-27
;  PRIOR APPLICATION NUMBER: 60/331,469
;  PRIOR FILING DATE: 2001-11-16
;  PRIOR APPLICATION NUMBER: 60/340,817
;  PRIOR FILING DATE: 2001-12-19
;  PRIOR APPLICATION NUMBER: 09/880,748
;  PRIOR FILING DATE: 2001-06-15
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  PRIOR APPLICATION NUMBER: 60/212,210
;  PRIOR FILING DATE: 2000-06-16
;  NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 479
;   LENGTH: 249
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-293-418-479

  Query Match           100.0%;  Score 640;  DB 12;  Length 249;
  Best Local Similarity  100.0%;  Pred. No. 8.8e-57;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60

Qy         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHYGMDVWGRGTMVT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHYGMDVWGRGTMVT 120

Qy        121 VSS 123
              |||
Db        121 VSS 123


RESULT 12
US-10-293-418-618
; Sequence 618, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523P2
;  CURRENT APPLICATION NUMBER: US/10/293,418
;  CURRENT FILING DATE:  2002-11-27
;  PRIOR APPLICATION NUMBER: 60/331,469
;  PRIOR FILING DATE: 2001-11-16
;  PRIOR APPLICATION NUMBER: 60/340,817
;  PRIOR FILING DATE: 2001-12-19
;  PRIOR APPLICATION NUMBER: 09/880,748
;  PRIOR FILING DATE: 2001-06-15
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  PRIOR APPLICATION NUMBER: 60/212,210
;  PRIOR FILING DATE: 2000-06-16
;  NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 618
;   LENGTH: 249
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-293-418-618

  Query Match           100.0%;  Score 640;  DB 12;  Length 249;
  Best Local Similarity  100.0%;  Pred. No. 8.8e-57;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60

Qy         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHYGMDVWGRGTMVT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHYGMDVWGRGTMVT 120

Qy        121 VSS 123
              |||
Db        121 VSS 123


RESULT 13
US-10-293-418-719
; Sequence 719, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523P2
;  CURRENT APPLICATION NUMBER: US/10/293,418
;  CURRENT FILING DATE:  2002-11-27
;  PRIOR APPLICATION NUMBER: 60/331,469
;  PRIOR FILING DATE: 2001-11-16
;  PRIOR APPLICATION NUMBER: 60/340,817
;  PRIOR FILING DATE: 2001-12-19
;  PRIOR APPLICATION NUMBER: 09/880,748
;  PRIOR FILING DATE: 2001-06-15
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  PRIOR APPLICATION NUMBER: 60/212,210
;  PRIOR FILING DATE: 2000-06-16
;  NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 719
;   LENGTH: 249
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-293-418-719
```

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  Query Match             100.0%;  Score 640;  DB 12;  Length 249;
  Best Local Similarity   100.0%;  Pred. No. 8.8e-57;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60

Qy         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHYGMDVWGRGTMVT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHYGMDVWGRGTMVT 120

Qy        121 VSS 123
              |||
Db        121 VSS 123


RESULT 14
[redacted]0-293-418-796
[redacted]quence 796, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523P2
;  CURRENT APPLICATION NUMBER: US/10/293,418
;  CURRENT FILING DATE:  2002-11-27
;  PRIOR APPLICATION NUMBER: 60/331,469
;  PRIOR FILING DATE: 2001-11-16
;  PRIOR APPLICATION NUMBER: 60/340,817
;  PRIOR FILING DATE: 2001-12-19
;  PRIOR APPLICATION NUMBER: 09/880,748
;  PRIOR FILING DATE: 2001-06-15
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  PRIOR APPLICATION NUMBER: 60/212,210
;  PRIOR FILING DATE: 2000-06-16
;  NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 796
;   LENGTH: 249
;   TYPE: PRT
[redacted]  ORGANISM: Homo sapiens
[redacted]10-293-418-796

  Query Match             100.0%;  Score 640;  DB 12;  Length 249;
  Best Local Similarity   100.0%;  Pred. No. 8.8e-57;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60

Qy         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHYGMDVWGRGTMVT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHYGMDVWGRGTMVT 120

Qy        121 VSS 123
              |||
Db        121 VSS 123


RESULT 15
US-09-880-748-1426
; Sequence 1426, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523
;  CURRENT APPLICATION NUMBER: US/09/880,748
;  CURRENT FILING DATE:  2001-06-15
;  PRIOR APPLICATION NUMBER: 60/212,210
;  PRIOR FILING DATE: 2000-06-15
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  NUMBER OF SEQ ID NOS: 3239
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1426
;   LENGTH: 246
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-880-748-1426

  Query Match             99.5%;  Score 637;  DB 10;  Length 246;
  Best Local Similarity   99.2%;  Pred. No. 1.8e-56;
  Matches  122;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60

Qy         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHYGMDVWGRGTMVT 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:||
Db         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHYGMDVWGRGTLVT 120

Qy        121 VSS 123
              |||
Db        121 VSS 123


Search completed: September  9, 2004, 11:23:42
Job time : 91.4103 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: September 9, 2004, 10:59:50 ; Search time 13.6667 Seconds
(without alignments)
865.724 Million cell updates/sec

Title: US-09-880-748-2_COPY_1_123
Perfect score: 640
Sequence: 1 QVQLQQSGAEVKKPGSSVRV.....LFPHYGMDVWGRGTMVTVSS 123

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 70 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	510	79.7	119	2	PH0961	Ig heavy chain V r
2	505.5	79.0	122	2	PH0958	Ig heavy chain V r
3	504.5	78.8	132	2	PH0954	Ig heavy chain V r
4	502	78.4	133	2	C33548	Ig heavy chain V-1
5	502	78.4	627	2	S14683	Ig mu chain precur
6	501.5	78.4	136	2	PH0960	Ig heavy chain V r
7	499.5	78.0	132	2	S46394	Ig heavy chain V r
8	498	77.8	127	2	PH0955	Ig heavy chain V r
9	494.5	77.3	126	2	B33548	Ig heavy chain V-1
10	491	76.7	135	2	PH0953	Ig heavy chain V r
11	490	76.6	129	2	A33548	Ig heavy chain V-1
12	489.5	76.5	120	2	PH0962	Ig heavy chain V r
13	485.5	75.9	128	2	PH0952	Ig heavy chain V r
14	483.5	75.5	116	2	PH0959	Ig heavy chain V r
15	480	75.0	125	2	PH0957	Ig heavy chain V r
16	475	74.2	122	2	B49590	Ig heavy chain V r
17	468.5	73.2	116	2	S36261	Ig heavy chain V r
18	463.5	72.4	135	2	B32274	Ig heavy chain pre
19	452	70.6	113	2	PH1663	Ig heavy chain V r
20	450.5	70.4	108	2	PH1664	Ig heavy chain V r
21	445	69.5	123	2	S44108	Ig heavy chain V-D
22	444	69.4	98	2	S26915	Ig heavy chain V r
23	444	69.4	116	2	S31698	Ig heavy chain pre
24	440	68.8	98	2	S24680	Ig heavy chain V1
25	439	68.6	121	2	A49590	Ig heavy chain V r
26	435	68.0	119	2	S44106	Ig heavy chain V-D
27	429	67.0	122	2	C49590	Ig heavy chain V r
28	427	66.7	117	1	G1HUEU	Ig heavy chain V-I
29	425	66.4	109	2	PH1671	Ig heavy chain V r
30	420.5	65.7	124	2	S19665	Ig heavy chain V r
31	419	65.5	129	2	S36260	Ig heavy chain V r
32	418	65.3	142	2	A32483	Ig heavy chain V r
33	416	65.0	98	2	A30523	Ig heavy chain V-I
34	416	65.0	98	2	S46463	Ig heavy chain V1
35	412.5	64.5	136	2	S31600	Ig heavy chain V r
36	411	64.2	116	2	S31667	Ig heavy chain V r
37	410.5	64.1	118	2	S36265	Ig heavy chain V r
38	408	63.7	97	2	PH0870	Ig heavy chain V r
39	404.5	63.2	119	2	F49590	Ig heavy chain V r
40	404.5	63.2	135	2	S49530	anti-Sm antibody V
41	400	62.5	123	2	D33548	Ig heavy chain V-1
42	397.5	62.1	118	2	PH1666	Ig heavy chain V r
43	397	62.0	127	2	S34014	Ig heavy chain V r
44	397	62.0	129	2	S46393	Ig heavy chain V r
45	394	61.6	160	2	PL0105	anti-PR2 erythrocy
46	391.5	61.2	114	2	PH1667	Ig heavy chain V r
47	390	60.9	121	2	S20783	Ig heavy chain V r
48	389	60.8	122	2	S36271	Ig heavy chain V r
49	388	60.6	148	2	S29257	Ig heavy chain V r
50	387.5	60.5	120	2	S31999	Ig heavy chain V r
51	387	60.5	131	2	S26792	Ig heavy chain V r
52	383.5	59.9	171	2	S23623	Ig heavy chain V r
53	382.5	59.8	104	2	PH1665	Ig heavy chain V r
54	379.5	59.3	143	1	E1HUND	Ig heavy chain pre
55	379	59.2	123	2	S20646	Ig heavy chain V r
56	379	59.2	142	2	S19245	Ig heavy chain pre
57	378.5	59.1	120	2	S26789	Ig heavy chain V r
58	377	58.9	138	2	E32513	Ig heavy chain pre
59	375.5	58.7	132	2	S31596	Ig heavy chain V r
60	374	58.4	117	1	HVHUHG	Ig heavy chain pre
61	372.5	58.2	139	2	PS0024	Ig heavy chain pre
62	372.5	58.2	469	2	S37483	Ig gamma-2a chain
63	372	58.1	138	2	PH1565	Ig heavy chain V r
64	372	58.1	138	2	S21810	Ig heavy chain V r
65	371	58.0	125	2	S68170	Ig heavy chain V r
66	370.5	57.9	119	2	A24672	Ig heavy chain pre
67	369	57.7	144	2	E41287	Ig heavy chain pre
68	368	57.5	98	2	S26920	Ig heavy chain V r
69	368	57.5	134	2	S21916	Ig heavy chain V r
70	367.5	57.4	136	2	A49047	Ig heavy chain V r

ALIGNMENTS

RESULT 1
PH0961
Ig heavy chain V region (G6+ T-L33) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C;Accession: PH0961
R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A;Title: Evidence for somatic selection of natural autoantibodies.
A;Reference number: PH0952; MUID:92202880; PMID:1552291
A;Accession: PH0961
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-119 <MAR>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-30/Region: framework 1
F;15-98/Domain: immunoglobulin homology <IMM>
F;31-35/Region: complementarity-determining 1
F;36-50/Region: framework 2
F;51-67/Region: complementarity-determining 2
F;68-98/Region: framework 3
F;99-107/Region: complementarity-determining 3

Query Match 79.7%; Score 510; DB 2; Length 119;
Best Local Similarity 81.3%; Pred. No. 3.1e-40;
Matches 100; Conservative 9; Mismatches 10; Indels 4; Gaps 1;

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Qy          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60
              |||| |||||||||||||:||||||||:: ||:||||||||||||||||:|||| |
Db          1 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY 60

Qy         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHYGMDVWGRGTMVT 120
              :| ||||| |||||||||| |||||||||||||||||      : :|||||:|| ||
Db         61 AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARG----YYYYYGMDVWGQGTTVT 116

Qy        121 VSS 123
              |||
Db        117 VSS 119


RESULT 2
PH0958
Ig heavy chain V region (G6+ CLL-HUR) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C;Accession: PH0958
R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A;Title: Evidence for somatic selection of natural autoantibodies.
A;Reference number: PH0952; MUID:92202880; PMID:1552291
A;Accession: PH0958
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-122 <MAR>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-30/Region: framework 1
F;15-98/Domain: immunoglobulin homology <IMM>
F;31-35/Region: complementarity-determining 1
F;36-50/Region: framework 2
F;51-67/Region: complementarity-determining 2
F;68-98/Region: framework 3
F;99-110/Region: complementarity-determining 3

  Query Match             79.0%;  Score 505.5;  DB 2;  Length 122;
  Best Local Similarity   82.1%;  Pred. No. 8.4e-40;
  Matches  101;  Conservative    8;  Mismatches   13;  Indels    1;  Gaps    1;

Qy          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60
              |||| |||||||||||||:||||||||:: ||:||||||||||||||||:|||| |
Db          1 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY 60

Qy         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHYGMDVWGRGTMVT 120
              :| ||||| |||||||||| |||||||||||||||||  : | |   ||||||:|| ||
Db         61 AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARVPNPLFFA-VGMDVWGQGTTVT 119

Qy        121 VSS 123
              |||
Db        120 VSS 122


RESULT 3
PH0954
Ig heavy chain V region (G6+ CLL-HEN) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C;Accession: PH0954
R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A;Title: Evidence for somatic selection of natural autoantibodies.
A;Reference number: PH0952; MUID:92202880; PMID:1552291
A;Accession: PH0954
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-132 <MAR>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-30/Region: framework 1
F;15-98/Domain: immunoglobulin homology <IMM>
F;31-35/Region: complementarity-determining 1
F;36-50/Region: framework 2
F;51-67/Region: complementarity-determining 2
F;68-98/Region: framework 3
F;99-120/Region: complementarity-determining 3

  Query Match             78.8%;  Score 504.5;  DB 2;  Length 132;
  Best Local Similarity   76.5%;  Pred. No. 1.1e-39;
  Matches  101;  Conservative   10;  Mismatches   12;  Indels    9;  Gaps    2;

Qy          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60
              |||| |||||||||||||:||||||||:: ||:||||||||||||||||:|||| |
Db          1 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY 60

Qy         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLL------LFP---HYGMD 111
              :| ||||| |||||||||| |||||||||||||||||    :       :|   :||||
Db         61 AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARPHASIDDFWSGYYPNYYYYGMD 120

Qy        112 VWGRGTMVTVSS 123
              |||:|| |||||
Db        121 VWGQGTTVTVSS 132


RESULT 4
C33548
Ig heavy chain V-1 region (783) - human
C;Species: Homo sapiens (man)
C;Date: 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change 16-Aug-1996
C;Accession: C33548
R;Kipps, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A.
Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989
A;Title: Developmentally restricted immunoglobulin heavy chain variable region gene expr
A;Reference number: A33548; MUID:89345575; PMID:2503826
A;Accession: C33548
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A;Molecule type: DNA
A;Residues: 1-133 <KIP>
A;Experimental source: the sequence was determined from the differentiated gene
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match             78.4%;  Score 502;  DB 2;  Length 133;
  Best Local Similarity   74.8%;  Pred. No. 1.9e-39;
  Matches  101;  Conservative   11;  Mismatches    9;  Indels   14;  Gaps    2;

Qy          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60
              |||| |||||||||||||:||||||||:: ||:||||||||||||||||:|||| |
Db          1 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY 60

Qy         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFP------------HY 108
              :| ||||| |||||||||| |||||||||||||||||::   :| |            :|
Db         61 AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCAKTG--ILGPYSSGWYPNSDYYYY 118

Qy        109 GMDVWGRGTMVTVSS 123
              ||||||:|| |||||
Db        119 GMDVWGQGTTVTVSS 133


RESULT 5
S14683
Ig mu chain precursor, membrane-bound (clone 201) - human
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 23-Jul-1999
C;Accession: S14683; S08047
R;Friedlander, R.M.; Nussenzweig, M.C.; Leder, P.
Nucleic Acids Res. 18, 4278, 1990
A;Title: Complete nucleotide sequence of the membrane form of the human IgM heavy chain
A;Reference number: S14683; MUID:90332450; PMID:2115996
A;Accession: S14683
A;Molecule type: mRNA
A;Residues: 1-627 <FRI>
A;Cross-references: EMBL:X17115; NID:g33450; PIDN:CAA34971.1; PID:g33451
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C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin; membrane protein
F;1-15/Domain: signal sequence #status predicted <SIG>
F;16-627/Product: Ig mu chain #status predicted <MAT>
F;34-117/Domain: immunoglobulin homology <IMM>

  Query Match            78.4%;  Score 502;  DB 2;  Length 627;
  Best Local Similarity  74.8%;  Pred. No. 1e-38;
  Matches  101;  Conservative   11;  Mismatches    9;  Indels   14;  Gaps    2;

Qy          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60
              |||| |||||||||||||:||||||||:: ||:||||||||||||||||:|||| |
Db         20 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY 79

Qy         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFP-----------HY 108
              :| ||||| |||||||||| ||||||||||||||||::   :| |          :|
Db         80 AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCAKTG--ILGPYSSGWYPNSDYYYY 137

Qy        109 GMDVWGRGTMVTVSS 123
              ||||||:|| |||||
Db        138 GMDVWGQGTTVTVSS 152


RESULT 6
PH0960
Ig heavy chain V region (G6+ T-L30) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C;Accession: PH0960
R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A;Title: Evidence for somatic selection of natural autoantibodies.
A;Reference number: PH0952; MUID:92202880; PMID:1552291
A;Accession: PH0960
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-136 <MAR>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-30/Region: framework 1
F;15-98/Domain: immunoglobulin homology <IMM>
F;31-35/Region: complementarity-determining 1
F;36-50/Region: framework 2
F;51-67/Region: complementarity-determining 2
F;68-98/Region: framework 3
F;99-124/Region: complementarity-determining 3

  Query Match            78.4%;  Score 501.5;  DB 2;  Length 136;
  Best Local Similarity  73.5%;  Pred. No. 2.2e-39;
  Matches  100;  Conservative   10;  Mismatches   13;  Indels   13;  Gaps    1;

Qy          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60
              |||| |||||||||||||:||||||||:: ||:||||||||||||||||:|||| |
Db          1 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY 60

Qy         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLL-------------LFPH 107
              :| ||||| ||||:||||| |||||||||||||||| |  :             :
Db         61 AQKFQGRVTITADKSTSTAYMELSSLRSEDTAVYYCARGRTRVSVSTLYDSSGYYDFSGY 120

Qy        108 YGMDVWGRGTMVTVSS 123
              |||||||:|| |||||
Db        121 YGMDVWGQGTTVTVSS 136


RESULT 7
S46394
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
C;Accession: S46394
R;Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.
J. Mol. Biol. 239, 68-78, 1994
A;Title: In vitro assembly of repertoires of antibody chains on the surface of phage by
A;Reference number: S46390; MUID:94254092; PMID:8196048
A;Accession: S46394
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-132 <PIG>
A;Cross-references: EMBL:Z31681; NID:g509788; PIDN:CAA83486.1; PID:g1335147
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match            78.0%;  Score 499.5;  DB 2;  Length 132;
  Best Local Similarity  75.8%;  Pred. No. 3.3e-39;
  Matches  100;  Conservative   12;  Mismatches   11;  Indels    9;  Gaps    1;

Qy          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60
              |||| |||||||||||||:||||||||:: ||:||||||||||||||||:|||| :
Db          1 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANH 60

Qy         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSR---------DLLLFPHYGMD 111
              :| ||||| |||||||||| ||||||||||||||||::         : |   :| ||
Db         61 AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARTQLPAADTGILEWLPSYYYYMD 120

Qy        112 VWGRGTMVTVSS 123
              |||:||||||||
Db        121 VWGKGTMVTVSS 132


RESULT 8
PH0955
Ig heavy chain V region (G6+ CLL-AND) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C;Accession: PH0955
R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A;Title: Evidence for somatic selection of natural autoantibodies.
A;Reference number: PH0952; MUID:92202880; PMID:1552291
A;Accession: PH0955
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-127 <MAR>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-30/Region: framework 1
F;15-98/Domain: immunoglobulin homology <IMM>
F;31-35/Region: complementarity-determining 1
F;36-50/Region: framework 2
F;51-67/Region: complementarity-determining 2
F;68-98/Region: framework 3
F;99-115/Region: complementarity-determining 3

  Query Match            77.8%;  Score 498;  DB 2;  Length 127;
  Best Local Similarity  78.7%;  Pred. No. 4.3e-39;
  Matches  100;  Conservative    8;  Mismatches   15;  Indels    4;  Gaps    1;

Qy          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60
              |||| |||||||||||||:||||||||:: ||:||||||||||||||||:|||| |
Db          1 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY 60

Qy         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPH----YGMDVWGRG 116
              :| ||||| |||||||||| ||||||||||||||||||     :  |    | |||||:|
Db         61 AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARVSIFGVVQHYYYYYYMDVWGKG 120

Qy        117 TMVTVSS 123
              | |||||
Db        121 TTVTVSS 127


RESULT 9
B33548
Ig heavy chain V-1 region (AND) - human
C;Species: Homo sapiens (man)
C;Date: 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change 16-Aug-1996
```

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C;Accession: B33548
R;Kipps, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A.
Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989
A;Title: Developmentally restricted immunoglobulin heavy chain variable region gene expr
A;Reference number: A33548; MUID:89345575; PMID:2503826
A;Accession: B33548
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A;Molecule type: DNA
A;Residues: 1-126 <KIP>
A;Experimental source: the sequence was determined from the differentiated gene
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match             77.3%;  Score 494.5;  DB 2;  Length 126;
  Best Local Similarity   79.4%;  Pred. No. 9e-39;
  Matches  100;  Conservative    7;  Mismatches   16;  Indels    3;  Gaps    1;

Qy          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60
              |||| |||||||||||||:||||||||:: ||:||||||||||||||||:|||| |
Db          1 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY 60

Qy         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPH---YGMDVWGRGT 117
              :| ||||| |||||||||| ||||||||||||||||     :  |   | ||||| ||
Db         61 AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARVSIFGVVQHYYYYYMDVWGLGT 120

Qy        118 MVTVSS 123
               |||||
Db        121 TVTVSS 126


RESULT 10
PH0953
Ig heavy chain V region (G6+ CLL-SIC) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C;Accession: PH0953
R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A;Title: Evidence for somatic selection of natural autoantibodies.
A;Reference number: PH0952; MUID:92202880; PMID:1552291
A;Accession: PH0953
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-135 <MAR>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-30/Region: framework 1
F;15-98/Domain: immunoglobulin homology <IMM>
F;31-35/Region: complementarity-determining 1
F;36-50/Region: framework 2
F;51-67/Region: complementarity-determining 2
F;68-98/Region: framework 3
F;99-123/Region: complementarity-determining 3

  Query Match             76.7%;  Score 491;  DB 2;  Length 135;
  Best Local Similarity   75.6%;  Pred. No. 2e-38;
  Matches  102;  Conservative    7;  Mismatches   14;  Indels   12;  Gaps    2;

Qy          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60
              |||| |||||||||||||:||||||||:: ||:||||||||||||||||:|||| |
Db          1 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY 60

Qy         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCAR---------SRDLLL---FPHY 108
              :| ||||| |||||||||| |||||||||||||||||          ||  ||   |
Db         61 AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARNGYCGGDCYSRWELLRFDFSED 120

Qy        109 GMDVWGRGTMVTVSS 123
               |:|| ||||||||
Db        121 AFDIWGPGTMVTVSS 135


RESULT 11
A33548
Ig heavy chain V-1 region (NEI) - human
C;Species: Homo sapiens (man)
C;Date: 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change 16-Aug-1996
C;Accession: A33548; PH0956
R;Kipps, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A.
Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989
A;Title: Developmentally restricted immunoglobulin heavy chain variable region gene expr
A;Reference number: A33548; MUID:89345575; PMID:2503826
A;Accession: A33548
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-129 <KIP>
R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A;Title: Evidence for somatic selection of natural autoantibodies.
A;Reference number: PH0952; MUID:92202880; PMID:1552291
A;Accession: PH0956
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-129 <MAR>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-30/Region: framework 1
F;15-98/Domain: immunoglobulin homology <IMM>
F;31-35/Region: complementarity-determining 1
F;36-50/Region: framework 2
F;51-67/Region: complementarity-determining 2
F;68-98/Region: framework 3
F;99-117/Region: complementarity-determining 3

  Query Match             76.6%;  Score 490;  DB 2;  Length 129;
  Best Local Similarity   76.3%;  Pred. No. 2.4e-38;
  Matches  100;  Conservative   11;  Mismatches   10;  Indels   10;  Gaps    3;

Qy          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60
              |||| |||||||||||||:||||||||:: ||:||||||||||||||||:|||| |
Db          1 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY 60

Qy         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARS----RDLLLFPHYG----MDV 112
              :| ||||| |||||||||| |||||||||||||||||      |:||:  :|     |
Db         61 AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARGPRLLADVLLW--FGELSEFDY 118

Qy        113 WGRGTMVTVSS 123
              ||:||:|||||
Db        119 WGQGTLVTVSS 129


RESULT 12
PH0962
Ig heavy chain V region (G6+ T-L42) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C;Accession: PH0962
R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A;Title: Evidence for somatic selection of natural autoantibodies.
A;Reference number: PH0952; MUID:92202880; PMID:1552291
A;Accession: PH0962
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-120 <MAR>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-30/Region: framework 1
F;15-98/Domain: immunoglobulin homology <IMM>
F;31-35/Region: complementarity-determining 1
F;36-50/Region: framework 2
F;51-67/Region: complementarity-determining 2
F;68-98/Region: framework 3
F;99-108/Region: complementarity-determining 3

  Query Match             76.5%;  Score 489.5;  DB 2;  Length 120;
```

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  Best Local Similarity   79.7%;  Pred. No. 2.5e-38;
  Matches   98;  Conservative   10;  Mismatches   12;  Indels    3;  Gaps    2;

Qy          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60
              |||| |||||||||||||:||||||||:: ||:||||||||||||||||:|||| |
Db          1 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY 60

Qy         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHYGMDVWGRGTMVT 120
              :| ||||| |||||||||| |||||||||||||||||    :   ||:  | ||:||:||
Db         61 AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARG-GVAGRPHF--DYWGQGTLVT 117

Qy        121 VSS 123
              |||
Db        118 VSS 120


RESULT 13
PH0952
Ig heavy chain V region (G6+ CLL-SMI) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C;Accession: PH0952
R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A;Title: Evidence for somatic selection of natural autoantibodies.
A;Reference number: PH0952; MUID:92202880; PMID:1552291
A;Accession: PH0952
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-128 <MAR>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-30/Region: framework 1
F;15-98/Domain: immunoglobulin homology <IMM>
F;31-35/Region: complementarity-determining 1
F;36-50/Region: framework 2
F;51-67/Region: complementarity-determining 2
F;68-98/Region: framework 3
F;99-116/Region: complementarity-determining 3

  Query Match             75.9%;  Score 485.5;  DB 2;  Length 128;
  Best Local Similarity   75.8%;  Pred. No. 6.2e-38;
  Matches   97;  Conservative   12;  Mismatches   14;  Indels    5;  Gaps    2;

Qy          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60
              |||| |||||||||||||:|||||||||:: ||:||||||||||||||||:|||| |
Db          1 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY 60

Qy         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDL-LLFPHY----GMDVWGR 115
              :| ||||| ||||:||||| |||||||||||||||||  :   ::  |      |:||:
Db         61 AQKFQGRVTITADKSTSTAYMELSSLRSEDTAVYYCARGGNYDYIWGSYRSNDAFDIWGQ 120

Qy        116 GTMVTVSS 123
              ||||||||
Db        121 GTMVTVSS 128


RESULT 14
PH0959
Ig heavy chain V region (G6+ T-L26) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C;Accession: PH0959
R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A;Title: Evidence for somatic selection of natural autoantibodies.
A;Reference number: PH0952; MUID:92202880; PMID:1552291
A;Accession: PH0959
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-116 <MAR>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-30/Region: framework 1
F;15-98/Domain: immunoglobulin homology <IMM>
F;31-35/Region: complementarity-determining 1
F;36-50/Region: framework 2
F;51-67/Region: complementarity-determining 2
F;68-98/Region: framework 3
F;99-104/Region: complementarity-determining 3

  Query Match             75.5%;  Score 483.5;  DB 2;  Length 116;
  Best Local Similarity   78.0%;  Pred. No. 8.6e-38;
  Matches   96;  Conservative    9;  Mismatches   11;  Indels    7;  Gaps    1;

Qy          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60
              |||| |||||||||||||:|||||||||:: ||:||||||||||||||||:|||| |
Db          1 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY 60

Qy         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHYGMDVWGRGTMVT 120
              :| ||||| |||||||||| |||||||||||||||||  :         | ||:||:||
Db         61 AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARGDN-------WFDPWGQGTLVT 113

Qy        121 VSS 123
              |||
Db        114 VSS 116


RESULT 15
PH0957
Ig heavy chain V region (G6+ CLL-BRA) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C;Accession: PH0957
R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A;Title: Evidence for somatic selection of natural autoantibodies.
A;Reference number: PH0952; MUID:92202880; PMID:1552291
A;Accession: PH0957
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-125 <MAR>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-30/Region: framework 1
F;15-98/Domain: immunoglobulin homology <IMM>
F;31-35/Region: complementarity-determining 1
F;36-50/Region: framework 2
F;51-67/Region: complementarity-determining 2
F;68-98/Region: framework 3
F;99-113/Region: complementarity-determining 3

  Query Match             75.0%;  Score 480;  DB 2;  Length 125;
  Best Local Similarity   78.0%;  Pred. No. 2e-37;
  Matches   99;  Conservative    9;  Mismatches   13;  Indels    6;  Gaps    3;

Qy          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60
              |||| |||||||||||||:|||||||||:: |||||||||||||||||||:|||| |
Db          1 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAINWVRQAPGQGLEWMGGIIPIFGTANY 60

Qy         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCAR---SRDLLLFPHYG-MDVWGRG 116
              :| ||||| ||||||||:|| ||||||||||||||||||    |      |  :|  | ||:|
Db         61 AQKFQGRVTITADESTNTAYMELSSLRSEDTAVYYCARDGCSGGSCYF--WGWFDPWGQG 118

Qy        117 TMVTVSS 123
              |:|||||
Db        119 TLVTVSS 125


Search completed: September  9, 2004, 11:07:24
Job time : 14.6667 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: September 9, 2004, 10:58:34 ; Search time 8.9359 Seconds
(without alignments)
716.730 Million cell updates/sec

Title: US-09-880-748-2_COPY_1_123
Perfect score: 640
Sequence: 1 QVQLQQSGAEVKKPGSSVRV.....LFPHYGMDVWGRGTMVTVSS 123

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 70 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	427	66.7	117	1	HV1A_HUMAN	P01742 homo sapien
2	379.5	59.3	147	1	HV1C_HUMAN	P01744 homo sapien
3	374	58.4	117	1	HV1B_HUMAN	P01743 homo sapien
4	359	56.1	120	1	HV03_MOUSE	P01747 mus musculu
5	356	55.6	140	1	HV02_MOUSE	P01746 mus musculu
6	353.5	55.2	139	1	HV07_MOUSE	P01751 mus musculu
7	350	54.7	117	1	HV13_MOUSE	P01757 mus musculu
8	349	54.5	117	1	HV1G_HUMAN	P23083 homo sapien
9	347	54.2	117	1	HV12_MOUSE	P01756 mus musculu
10	345.5	54.0	114	1	HV00_MOUSE	P01741 mus musculu
11	344.5	53.8	118	1	HV51_MOUSE	P06330 mus musculu
12	341	53.3	121	1	HV01_MOUSE	P01745 mus musculu
13	341	53.3	138	1	HV48_MOUSE	P03980 mus musculu
14	338.5	52.9	120	1	HV1H_HUMAN	P80421 homo sapien
15	338.5	52.9	137	1	HV11_MOUSE	P01755 mus musculu
16	330.5	51.6	120	1	HV50_MOUSE	P06329 mus musculu
17	329	51.4	125	1	HV1F_HUMAN	P06326 homo sapien
18	328.5	51.3	124	1	HV1D_HUMAN	P01760 homo sapien
19	328	51.2	117	1	HV52_MOUSE	P06327 mus musculu
20	318.5	49.8	124	1	HV1E_HUMAN	P01761 homo sapien
21	314	49.1	117	1	HV05_MOUSE	P01749 mus musculu
22	313	48.9	136	1	HV15_MOUSE	P01759 mus musculu
23	311	48.6	117	1	HV06_MOUSE	P01750 mus musculu
24	309	48.3	121	1	HV3J_HUMAN	P01771 homo sapien
25	308	48.1	117	1	HV04_MOUSE	P01748 mus musculu
26	308	48.1	117	1	HV09_MOUSE	P01753 mus musculu
27	307.5	48.0	122	1	HV3G_HUMAN	P01768 homo sapien
28	305	47.7	119	1	HV3I_HUMAN	P01770 homo sapien
29	303	47.3	117	1	HV49_MOUSE	P06328 mus musculu
30	301	47.0	117	1	HV14_MOUSE	P01758 mus musculu
31	300	46.9	117	1	HV10_MOUSE	P01754 mus musculu
32	299.5	46.8	136	1	HV16_MOUSE	P01783 mus musculu
33	295.5	46.2	114	1	HV3B_HUMAN	P01763 homo sapien
34	295	46.1	115	1	HV3D_HUMAN	P01765 homo sapien
35	292.5	45.7	122	1	HV3H_HUMAN	P01769 homo sapien
36	291	45.5	117	1	HV42_MOUSE	P01812 mus musculu
37	287.5	44.9	119	1	HV38_MOUSE	P01808 mus musculu
38	284.5	44.5	146	1	HV2I_HUMAN	P06331 homo sapien
39	281.5	44.0	119	1	HV40_MOUSE	P01810 mus musculu
40	280	43.8	123	1	HV22_MOUSE	P01791 mus musculu
41	279.5	43.7	116	1	HV3T_HUMAN	P01781 homo sapien
42	278	43.4	117	1	HV02_CANFA	P01785 canis famil
43	277.5	43.4	126	1	HV3K_HUMAN	P01772 homo sapien
44	276.5	43.2	119	1	HV37_MOUSE	P01807 mus musculu
45	275.5	43.0	122	1	HV3A_HUMAN	P01762 homo sapien
46	275	43.0	115	1	HV3F_HUMAN	P01767 homo sapien
47	275	43.0	120	1	HV3E_HUMAN	P01766 homo sapien
48	273	42.7	117	1	HV41_MOUSE	P01811 mus musculu
49	270.5	42.3	119	1	HV3P_HUMAN	P01777 homo sapien
50	267.5	41.8	120	1	HV3U_HUMAN	P01782 homo sapien
51	266	41.6	116	1	HV3R_HUMAN	P01779 homo sapien
52	266	41.6	117	1	HV3C_HUMAN	P01764 homo sapien
53	264.5	41.3	122	1	HV21_MOUSE	P01790 mus musculu
54	264	41.2	117	1	HV2G_HUMAN	P01825 homo sapien
55	264	41.2	142	1	HV01_RAT	P01805 rattus norv
56	263.5	41.2	118	1	HV3V_HUMAN	P80419 homo sapien
57	263.5	41.2	122	1	HV20_MOUSE	P01789 mus musculu
58	263	41.1	123	1	HV18_MOUSE	P01787 mus musculu
59	263	41.1	123	1	HV19_MOUSE	P01788 mus musculu
60	262	40.9	123	1	HV25_MOUSE	P01794 mus musculu
61	261	40.8	113	1	HV30_MOUSE	P01799 mus musculu
62	261	40.8	115	1	HV32_MOUSE	P01801 mus musculu
63	261	40.8	123	1	HV23_MOUSE	P01792 mus musculu
64	259.5	40.5	114	1	HV01_CANFA	P01784 canis famil
65	259	40.5	118	1	HV39_MOUSE	P01809 mus musculu
66	259	40.5	129	1	HV2F_HUMAN	P01824 homo sapien
67	258	40.3	116	1	HV3Q_HUMAN	P01778 homo sapien
68	258	40.3	119	1	HV3L_HUMAN	P01773 homo sapien
69	257.5	40.2	111	1	HV35_MOUSE	P01804 mus musculu
70	257.5	40.2	115	1	HV3S_HUMAN	P01780 homo sapien

ALIGNMENTS

RESULT 1
HV1A_HUMAN
ID HV1A_HUMAN STANDARD; PRT; 117 AA.
AC P01742;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-I region EU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=71064024; PubMed=5489771;
RA Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,
RA Waxdal M.J., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. VII. Amino
RT acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";
RL Biochemistry 9:3161-3170(1970).
RN [2]
RP DISULFIDE BOND.
RX MEDLINE=71064027; PubMed=4923144;
RA Gall W.E., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. X.
RT Intrachain disulfide bonds.";
RL Biochemistry 9:3188-3196(1970).
CC -!- MISCELLANEOUS: THE SEQUENCE OF THE GAMMA-1 C REGION OF THIS
CC MYELOMA PROTEIN HAS ALSO BEEN DETERMINED.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A90563; G1HUEU.

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DR   HSSP; P01772; 2FB4.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Pyrrolidone carboxylic acid.
FT   DOMAIN        1    112       IG-LIKE.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   DISULFID     22     96
FT   NON_TER     117    117
SQ   SEQUENCE   117 AA;  12472 MW;  99D60ADAEBD52818 CRC64;

  Query Match             66.7%;  Score 427;  DB 1;  Length 117;
  Best Local Similarity   70.7%;  Pred. No. 1.1e-37;
  Matches   87;  Conservative    9;  Mismatches   21;  Indels    6;  Gaps    1;

Qy          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60
              |||| |||||||||||||:||||||||||: :|| |||||||||||||||:||||    |
Db          1 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSRSAIIWVRQAPGQGLEWMGGIVPMFGPPNY 60

Qy         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHYGMDVWGRGTMVT 120
              :| ||||| |||||||:|| |||||||||||| |:||    :      |        | :||
Db         61 AQKFQGRVTITADESTNTAYMELSSLRSEDTAFYFCAGGYGIYSPEEY------NGGLVT 114

Qy        121 VSS 123
              |||
Db        115 VSS 117


RESULT 2
HV1C_HUMAN
ID   HV1C_HUMAN     STANDARD;      PRT;   147 AA.
AC   P01744;
DT   21-JUL-1986 (Rel. 01, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig heavy chain V-I region ND precursor (Fragments).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=83065234; PubMed=6815656;
RA   Kenten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J.,
RA   Bell L.O., Gould H.J.;
RT   "Cloning and sequence determination of the gene for the human
RT   immunoglobulin epsilon chain expressed in a myeloma cell line.";
RL   Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).
RN   [2]
RP   SEQUENCE OF 20-147.
RA   Bennich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;
RL   (In) Bach M.K. (eds.);
RL   Immediate hypersensitivity: modern concepts and developments, pp.1-36,
RL   Marcel Dekker, New York (1978).
CC   -!- MISCELLANEOUS: THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA
CC       PROTEIN.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   HSSP; P01789; 1MCP.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal; Pyrrolidone carboxylic acid.
FT   SIGNAL        1     19
FT   CHAIN        20    147       IG HEAVY CHAIN V-I REGION ND.
FT   DOMAIN       20    131       IG-LIKE.
FT   MOD_RES      20     20       PYRROLIDONE CARBOXYLIC ACID.
FT   DISULFID     41    115
FT   CONFLICT     21     21       T -> V (IN REF. 2).
FT   CONFLICT     53     54       IH -> HI (IN REF. 2).
FT   CONFLICT     67     68       VG -> GV (IN REF. 2).
FT   CONFLICT    125    125       MISSING (IN REF. 2).
FT   NON_TER     147    147
SQ   SEQUENCE   147 AA;  16491 MW;  948F9F72A5366C20 CRC64;

  Query Match             59.3%;  Score 379.5;  DB 1;  Length 147;
  Best Local Similarity   60.9%;  Pred. No. 1.3e-32;
  Matches   78;  Conservative   17;  Mismatches   28;  Indels    5;  Gaps    2;

Qy          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60
              | || ||||||:|||:|||||||||| || :: |:|:||||| ||||:| | |  |   |
Db         20 QTQLVQSGAEVRKPGASVRVSCKASGYTFIDSYIHWIRQAPGHGLEWVGWINPNSGGTNY 79

Qy         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARS----RDLLLFPH-YGMDVWGR 115
              :  ||||| :| | | ||| |:| ||||:|:||:|||:|     |   | : | :||||: '
Db         80 APRFQGRVTMTRDASFSTAYMDLRSLRSDDSAVFYCAKSDPFWSDYYNFDYSYTLDVWGQ 139

Qy        116 GTMVTVSS 123
              || |||||
Db        140 GTTVTVSS 147


RESULT 3
HV1B_HUMAN
ID   HV1B_HUMAN     STANDARD;      PRT;   117 AA.
AC   P01743;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig heavy chain V-I region HG3 precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=83144028; PubMed=6298778;
RA   Rechavi G., Ram D., Glazer L., Zakut R., Givol D.;
RT   "Evolutionary aspects of immunoglobulin heavy chain variable region
RT   (VH) gene subgroups.";
RL   Proc. Natl. Acad. Sci. U.S.A. 80:855-859(1983).
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; J00240; AAA52988.1; -.
DR   PIR; A02024; HVHUHG.
DR   HSSP; P01772; 2FB4.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    117       IG HEAVY CHAIN V-I REGION HG3.
FT   DOMAIN       20   >117       IG-LIKE.
FT   NON_TER     117    117
SQ   SEQUENCE   117 AA;  12946 MW;  2D3F92FC60CD1FE7 CRC64;
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  Query Match             58.4%;  Score 374;  DB 1;  Length 117;
  Best Local Similarity   75.5%;  Pred. No. 3.8e-32;
  Matches   74;  Conservative    8;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60
              |||| |||||||||||:||:||||||| |||:  ::|||||||||||||| | |  |: |
Db         20 QVQLVQSGAEVKKPGASVKVSCKASGYTFNSYYMHWVRQAPGQGLEWMGIINPSGGSTSY 79

Qy         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCAR 98
              :| ||||| :| | ||||  ||||||||||||||||||
Db         80 AQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAR 117


RESULT 4
HV03_MOUSE
ID   HV03_MOUSE     STANDARD;      PRT;   120 AA.
AC   P01747;
     21-JUL-1986 (Rel. 01, Created)
     21-JUL-1986 (Rel. 01, Last sequence update)
     10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig heavy chain V region 36-65.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=83131846; PubMed=6186498;
RA   Siekevitz M., Gefter M.L., Brodeur P., Riblet R.,
RA   Marshak-Rothstein A.;
RT   "The genetic basis of antibody production: the dominant anti-arsonate
RT   idiotype response of the strain A mouse.";
RL   Eur. J. Immunol. 12:1023-1032(1982).
CC   -!- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER
CC       DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS
CC       CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
CC       SEGMENT, JH2.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   HSSP; P01789; 1MCP.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Hybridoma.
FT   DOMAIN        1    111       IG-LIKE.
FT   NON_TER     120    120
SQ   SEQUENCE   120 AA;  13307 MW;  FF04E4A167B654AF CRC64;

  Query Match             56.1%;  Score 359;  DB 1;  Length 120;
  Best Local Similarity   57.1%;  Pred. No. 1.4e-30;
  Matches   72;  Conservative   20;  Mismatches   24;  Indels   10;  Gaps    2;

Qy          2 VQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKYS 61
              |||||||||: : ||||::|||||| || :  ||||:| |||||||:| | |  |  ||:
Db          1 VQLQQSGAELVRAGSSVKMSCKASGYTFTSYGINWVKQRPGQGLEWIGYINPGNGYTKYN 60

Qy         62 QNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHYG----MDVWGRGT 117
              : |:|:  :| |:|:||| |:| || |||:|||:|||       :||     | ||:||
Db         61 EKFKGKTTLTVDKSSSTAYMQLRSLTSEDSAVYFCARS------VYYGGSYYFDYWGQGT 114

Qy        118 MVTVSS 123
                :||||
Db        115 TLTVSS 120


RESULT 5
HV02_MOUSE
ID   HV02_MOUSE     STANDARD;      PRT;   140 AA.
AC   P01746;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig heavy chain V region 93G7 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=A/J;
RX   MEDLINE=82152818; PubMed=6801765;
RA   Sims J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.,
RA   Capra J.D.;
RT   "Somatic mutation in genes for the variable portion of the
RT   immunoglobulin heavy chain.";
RL   Science 216:309-311(1982).
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; J00493; AAA38128.1; -.
DR   PIR; A94264; HVMSG7.
DR   HSSP; P01810; 2FBJ.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Hybridoma; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    140       IG HEAVY CHAIN V REGION 93G7.
FT   DOMAIN       20    139       IG-LIKE.
FT   NON_TER     140    140
SQ   SEQUENCE   140 AA;  15514 MW;  25A4CBBE31DA5CE8 CRC64;

  Query Match             55.6%;  Score 356;  DB 1;  Length 140;
  Best Local Similarity   55.9%;  Pred. No. 3.5e-30;
  Matches   71;  Conservative   21;  Mismatches   25;  Indels   10;  Gaps    2;

Qy          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60
              :|||||||||: : ||||::||||||| || :  ||||:| |||||||:| | |  |   |
Db         20 EVQLQQSGAELVRAGSSVKMSCKASGYTFTSYGINWVKQRPGQGLEWIGYINPGNGYINY 79

Qy         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHYG----MDVWGRG 116
              :: |:|:  :| |:|:||| |:| || |||:|||:||||       :||     | ||:|
Db         80 NEKFKGKTTLTVDKSSSTAYMQLRSLTSEDSAVYFCARSH------YYGGSYDPDYWGQG 133

Qy        117 TMVTVSS 123
                | :||||
Db        134 TPLTVSS 140


RESULT 6
HV07_MOUSE
ID   HV07_MOUSE     STANDARD;      PRT;   139 AA.
AC   P01751; P01752;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig heavy chain V region B1-8/186-2 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RX   MEDLINE=81234548; PubMed=6788376;
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RA   Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA   Baltimore D.;
RT   "Heavy chain variable region contribution to the NPb family of
RT   antibodies: somatic mutation evident in a gamma 2a variable region.";
RL   Cell 24:625-637(1981).
CC   -!- MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC       MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC       (NPB ANTIBODIES).
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; J00529; AAA38170.1; -.
DR   PIR; A90809; MHMS18.
DR   PDB; 1A6U; 27-MAY-98.
DR   PDB; 1A6W; 15-JUL-98.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal; 3D-structure.
FT   SIGNAL        1     19
FT   CHAIN        20    139       IG HEAVY CHAIN V REGION B1-8/186-2.
FT   DOMAIN       20     49       FRAMEWORK-1.
FT   DOMAIN       50     54       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       55     68       FRAMEWORK-2.
FT   DOMAIN       69     85       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       86    117       FRAMEWORK-3.
FT   DOMAIN      118    124       D SEGMENT.
FT   DOMAIN      125    139       JH2 SEGMENT.
FT   DISULFID     41    115       BY SIMILARITY.
FT   NON_TER     139    139
SQ   SEQUENCE   139 AA;  15419 MW;  1B57DD4FD0C9F465 CRC64;

  Query Match             55.2%;  Score 353.5;  DB 1;  Length 139;
  Best Local Similarity   54.8%;  Pred. No. 6.3e-30;
  Matches   69;  Conservative   23;  Mismatches   25;  Indels    9;  Gaps    2;

Qy          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60
              |||||| |||: |||:||::|||||| || :  ::||:| ||:||||:| | |  |  ||
Db         20 QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGRGLEWIGRIDPNSGGTKY 79

           61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHYG---MDVWGRGT 117
              :: |: :  :| |: :||| |:|||| |||:|||||||      : :||    | ||:||
Db         80 NEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYYCAR------YDYYGSSYFDYWGQGT 133

Qy        118 MVTVSS 123
               :||||
Db        134 TLTVSS 139


RESULT 7
HV13_MOUSE
ID   HV13_MOUSE     STANDARD;      PRT;   117 AA.
AC   P01757;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig heavy chain V region J558.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=80078170; PubMed=6765983;
RA   Schilling J., Clevinger B., Davie J.M., Hood L.;
RT   "Amino acid sequence of homogeneous antibodies to dextran and DNA
RT   rearrangements in heavy chain V-region gene segments.";
RL   Nature 283:35-40(1980).
CC   -!- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO
CC       BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF
CC       WHICH OCCUR IN THE D AND J SEGMENTS.
CC   -!- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A26242; MHMSJ5.
DR   HSSP; P01789; 1MCP.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region.
FT   DOMAIN        1    116       IG-LIKE.
FT   DISULFID     22     96       BY SIMILARITY.
FT   NON_TER     117    117
SQ   SEQUENCE   117 AA;  13024 MW;  292E2AF4BE447E41 CRC64;

  Query Match             54.7%;  Score 350;  DB 1;  Length 117;
  Best Local Similarity   55.3%;  Pred. No. 1.2e-29;
  Matches   68;  Conservative   22;  Mismatches   27;  Indels    6;  Gaps    1;

Qy          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60
              :|||||| |: |||:||::|||||| || :  : ||:|: |: |||:| | |  |   |
Db          1 EVQLQQSGPELVKPGASVKMSCKASGYTFTDYYMKWVKQSHGKSLEWIGDINPNNGGTSY 60

Qy         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHYGMDVWGRGTMVT 120
              :| |:|:  :| |:|:|:|| |:|:|| |||:||||||| |      ::  |||| || ||
Db         61 NQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCARDR------YWYFDVWGAGTTVT 114

Qy        121 VSS 123
               |||
Db        115 VSS 117


RESULT 8
HV1G_HUMAN
ID   HV1G_HUMAN     STANDARD;      PRT;   117 AA.
AC   P23083;
DT   01-NOV-1991 (Rel. 20, Created)
DT   01-NOV-1991 (Rel. 20, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig heavy chain V-I region V35 precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88296408; PubMed=2841108;
RA   Matsuda F., Lee K.H., Nakai S., Sato T., Kodaira M., Zong S.Q.,
RA   Ohno H., Fukuhara S., Honjo T.;
RT   "Dispersed localization of D segments in the human immunoglobulin
RT   heavy-chain locus.";
RL   EMBO J. 7:1047-1051(1988).
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC   ---------------------------------------------------------------------
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CC   modified and this statement is not removed. Usage by and for commercial
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X07448; -; NOT_ANNOTATED_CDS.
DR   PIR; S00476; HVHU35.
DR   HSSP; P01772; 2FB4.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
```

```
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    117       IG HEAVY CHAIN V-I REGION V35.
FT   DOMAIN       20   >117       IG-LIKE.
FT   NON_TER     117    117
SQ   SEQUENCE   117 AA;  13009 MW;  BE61CE63F8CE97BD CRC64;

  Query Match             54.5%;  Score 349;  DB 1;  Length 117;
  Best Local Similarity   71.4%;  Pred. No. 1.5e-29;
  Matches   70;  Conservative    6;  Mismatches   22;  Indels    0;  Gaps    0;

Qy          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60
              |||| |||||||||||:||:||||||| ||    ::|||||||||||||| | |   |   |
Db         20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGRINPNSGGTNY 79

Qy         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCAR 98
              :| |||||  | | | ||| |||| |||:|| ||||||
Db         80 AQKFQGRVTSTRDTSISTAYMELSRLRSDDTVVYYCAR 117


RESULT 9
HV12_MOUSE
ID   HV12_MOUSE     STANDARD;      PRT;   117 AA.
AC   P01756;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig heavy chain V region MOPC 104E.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE ASN-55.
RX   MEDLINE=83075344; PubMed=6816276;
RA   Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
RA   Hood L.E.;
RT   "Complete amino acid sequence of a mouse mu chain: homology among
RT   heavy chain constant region domains.";
RL   Biochemistry 21:5415-5424(1982).
CC   -!- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA
CC       PROTEIN HAS ALSO BEEN DETERMINED.
CC   -!- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A02039; MHMS4E.
DR   HSSP; P01789; 1MCP.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Glycoprotein.
FT   DOMAIN        1    116       IG-LIKE.
FT   DISULFID     22     96       BY SIMILARITY.
FT   CARBOHYD     55     55       N-LINKED (GLCNAC. . .) (COMPLEX).
FT   NON_TER     117    117
SQ   SEQUENCE   117 AA;  12983 MW;  3CF8ACE4BE447E41 CRC64;

  Query Match             54.2%;  Score 347;  DB 1;  Length 117;
  Best Local Similarity   55.3%;  Pred. No. 2.5e-29;
  Matches   68;  Conservative   21;  Mismatches   28;  Indels    6;  Gaps    1;

Qy          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60
              :|||||||| |: |||:||::|||||| || :  : ||:|: |: |||:| | |   |   |
Db          1 EVQLQQSGPELVKPGASVKMSCKASGYTFTDYYMKWVKQSHGKSLEWIGDINPNNGGTSY 60

Qy         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHYGMDVWGRGTMVT 120
              :| |:|:  :| |:|:||| |:|:|| |||:|||||||  |      :  |||| || ||
Db         61 NQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCARDYD------WYFDVWGAGTTVT 114

Qy        121 VSS 123
              |||
Db        115 VSS 117


RESULT 10
HV00_MOUSE
ID   HV00_MOUSE     STANDARD;      PRT;   114 AA.
AC   P01741;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig heavy chain V region (Anti-arsonate antibody).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE.
RC   STRAIN=A/J;
RX   MEDLINE=79195438; PubMed=109536;
RA   Capra J.D., Nisonoff A.;
RT   "Structural studies on induced antibodies with defined idiotypic
RT   specificities. VII. The complete amino acid sequence of the heavy
RT   chain variable region of anti-p-azophenylarsenate antibodies from A/J
RT   mice bearing a cross-reactive idiotype.";
RL   J. Immunol. 123:279-284(1979).
CC   -!- MISCELLANEOUS: ANTIBODY ISOLATED FROM TEN MICE WAS EXCLUSIVELY OF
CC       THE IGG1 SUBCLASS. THERE WAS NO HETEROGENEITY IN THE HEAVY CHAIN V
CC       REGION SEQUENCE.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A02022; G1MSAA.
DR   HSSP; P01772; 2FB4.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region.
FT   DOMAIN        1    106       IG-LIKE.
FT   NON_TER     114    114
SQ   SEQUENCE   114 AA;  12555 MW;  99DD8F0B6A69F4BE CRC64;

  Query Match             54.0%;  Score 345.5;  DB 1;  Length 114;
  Best Local Similarity   61.3%;  Pred. No. 3.4e-29;
  Matches   73;  Conservative   16;  Mismatches   25;  Indels    5;  Gaps    2;

Qy          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60
              :|||||||||: | ||||::||||:| ||::  : |||||||||| :| |         |
Db          1 EVQLQQSGAELVKAGSSVKMSCKATGYTFSSYELYWVRQAPGQGLEDLGYISSSSAYPNY 60

Qy         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHYGMDVWGRGTMV 119
              :| ||||| |||||||:|| ||||||||||||||:||    : :   |  | ||:||:|
Db         61 AQKFQGRVTITADESTNTAYMELSSLRSEDTAVYFCA----VRVISRY-FDGWGQGTLV 114


RESULT 11
HV51_MOUSE
ID   HV51_MOUSE     STANDARD;      PRT;   118 AA.
AC   P06330;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V region AC38 205.12.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE.
```

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RX   MEDLINE=84182519; PubMed=6201362;
RA   Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
RT   "A V region determinant (idiotope) expressed at high frequency in B
RT   lymphocytes is encoded by a large set of antibody structural genes.";
RL   EMBO J. 3:517-523(1984).
DR   PIR; A02040; MHMS38.
DR   HSSP; P01789; 1MCP.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region.
FT   DOMAIN        1     98       V SEGMENT.
FT   DOMAIN       99    104       D SEGMENT.
FT   DOMAIN      105    118       J SEGMENT.
FT   DISULFID     22     96       BY SIMILARITY.
FT   NON_TER     118    118
SQ   SEQUENCE   118 AA;  12934 MW;  94F7BEE4C762A018 CRC64;

  Query Match             53.8%;  Score 344.5;  DB 1;  Length 118;
  Best Local Similarity   54.8%;  Pred. No. 4.6e-29;
  Matches   69;  Conservative   18;  Mismatches   28;  Indels   11;  Gaps    2;

Qy          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60
              :|||||| |: |||:||::|||||| || :  :|||:|: |: |||:| | |   |    |
Db          1 EVQLQQSGPELVKPGASVKISCKASGYTFTDYYMNWVKQSHGKSLEWIGDINPNNGGTSY 60

Qy         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHYG---MDVWGRGT 117
              :| |:|:  :| |:|:|   ||| || |||:|||||||         ||    |||| ||
Db         61 NQKFKGKATLTVDKSSSATYMELRSLTSEDSAVYYCARG--------YGYDPFDVWGTGT 112

Qy        118 MVTVSS 123
               |||||
Db        113 TVTVSS 118


RESULT 12
HV01_MOUSE
ID   HV01_MOUSE     STANDARD;      PRT;   121 AA.
AC   P01745;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig heavy chain V region MPC 11.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
     NCBI_TaxID=10090;
     [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=81053741; PubMed=6253904;
RA   Zakut R., Cohen J., Givol D.;
RT   "Cloning and sequence of the cDNA corresponding to the variable
RT   region of immunoglobulin heavy chain MPC11.";
RL   Nucleic Acids Res. 8:3591-3601(1980).
RN   [2]
RP   REVISIONS.
RA   Zakut R., Cohen J., Givol D.;
RL   Nucleic Acids Res. 8:4839-4840(1980).
CC   -!- MISCELLANEOUS: THIS SEQUENCE WAS TRANSLATED FROM AN MRNA ISOLATED
CC       FROM A MYELOMA THAT SECRETES IGG2B.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A93708; GVMS11.
DR   HSSP; P01810; 2FBJ.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region.
FT   DOMAIN        1    112       IG-LIKE.
FT   NON_TER     121    121

SQ   SEQUENCE   121 AA;  13135 MW;  227AEF3EC56ED0BF CRC64;

  Query Match             53.3%;  Score 341;  DB 1;  Length 121;
  Best Local Similarity   52.8%;  Pred. No. 1.1e-28;
  Matches   65;  Conservative   24;  Mismatches   32;  Indels    2;  Gaps    1;

Qy          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60
              : |||||||: :||:||::||||:| || |  | ||:: || ||||:| | |  |   |
Db          1 EAQLQQSGAELVRPGTSVKISCKAAGYTFTNYWIGWVKERPGHGLEWIGDIYPGGGFTNY 60

Qy         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHYGMDVWGRGTMVT 120
              : | :|:  :||| |:||| ::|||| |||:|:|:|||       |::  | ||:|| :|
Db         61 NDNLKGKATLTADTSSSTAYIQLSSLTSEDSAIYHCARGIYYNSSPYF--DSWGQGTTLT 118

Qy        121 VSS 123
               |||
Db        119 VSS 121


RESULT 13
HV48_MOUSE
ID   HV48_MOUSE     STANDARD;      PRT;   138 AA.
AC   P03980;
DT   23-OCT-1986 (Rel. 02, Created)
DT   23-OCT-1986 (Rel. 02, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V region TEPC 1017 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=84248078; PubMed=6429663;
RA   Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,
RA   Tucker P.W.;
RT   "Illegitimate recombination generates a class switch from C mu to C
RT   delta in an IgD-secreting plasmacytoma.";
RL   Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).
DR   PIR; A02033; HVMST7.
DR   HSSP; P01810; 2FBJ.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     20
FT   CHAIN        21    138       IG HEAVY CHAIN V REGION TEPC 1017.
FT   DOMAIN       21     49       FRAMEWORK-1.
FT   DOMAIN       50     54       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       55     68       FRAMEWORK-2.
FT   DOMAIN       69     85       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       86    117       FRAMEWORK-3.
FT   DOMAIN      118    127       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN      128    138       FRAMEWORK-4.
FT   DISULFID     41    115       BY SIMILARITY.
FT   NON_TER     138    138
SQ   SEQUENCE   138 AA;  15576 MW;  748157E4C6907B8E CRC64;

  Query Match             53.3%;  Score 341;  DB 1;  Length 138;
  Best Local Similarity   55.6%;  Pred. No. 1.3e-28;
  Matches   69;  Conservative   21;  Mismatches   28;  Indels    6;  Gaps    2;

Qy          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60
              |||||| |||: |||:||::|||||| || |  |:||:| |||||||:| | |  | : |
Db         20 QVQLQQPGAELVKPGASVQLSCKASGHTFTNYWIHWVKQRPGQGLEWIGEINPNDGRSNY 79

Qy         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHYGMDV-WGRGTMV 119
              :: |: :  :| |:|:||| |:|||  |: ||||||||       :|   | ||:||:|
Db         80 NEKFKNKATLTVDKSSSTAYMQLSSLTPEEFAVYYCARSDG-----YYDWFVYWGQGTLV 134

Qy        120 TVSS 123
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           | |:
Db        135 TFSA 138


RESULT 14
HV1H_HUMAN
ID   HV1H_HUMAN     STANDARD;      PRT;   120 AA.
AC   P80421;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig heavy chain V-I region DOT.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=95255298; PubMed=7737190;
RA   Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;
RT   "Characterization of the two unique human anti-flavin monoclonal
RT   immunoglobulins.";
RL   Eur. J. Biochem. 228:886-893(1995).
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   HSSP; P01772; 2FB4.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region.
FT   DOMAIN        1    111       IG-LIKE.
FT   DISULFID     22     95       BY SIMILARITY.
FT   NON_TER     120    120
SQ   SEQUENCE   120 AA;  13272 MW;  F1307FD253A782F1 CRC64;

  Query Match             52.9%;  Score 338.5;  DB 1;  Length 120;
  Best Local Similarity   58.5%;  Pred. No. 2e-28;
  Matches   72;  Conservative   16;  Mismatches   30;  Indels    5;  Gaps    3;

Qy          2 VQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKYS 61
              ||| ||| | | ||:|||:|||||| | |  |:||||||| ||||||    |: | | |
Db          2 VQLVQSGVERKVPGASVRISCKASGYAFENYYIHWVRQAPGLGLEWMGIFNPVAG-AVSS 60

Qy         62 QNFQGRVAITADESTSTASMELSSLRSEDTAVYYCAR-SRDLLLFPHYGMDVWGRGTMVT 120
              : |: |: :::| | :| ||:| :|||:||  |:||| | |   |  |||||||:|| |
Db         61 EKFRDRLVMSSDTSANTVSMQLRNLRSDDTGRYFCARVSYD---FSQYGMDVWGQGTTVI 117

Qy        121 VSS 123
             |||
Db        118 VSS 120


RESULT 15
HV11_MOUSE
ID   HV11_MOUSE     STANDARD;      PRT;   137 AA.
AC   P01755;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V region S43 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=81234548; PubMed=6788376;
RA   Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA   Baltimore D.;
RT   "Heavy chain variable region contribution to the NPb family of
RT   antibodies: somatic mutation evident in a gamma 2a variable region.";
RL   Cell 24:625-637(1981).
CC   -!- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC       MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC       (NPB ANTIBODIES).
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   use by non-profit institutions as long as its content is in no way
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; J00539; AAA38172.1; -.
DR   PIR; A02038; G2MS43.
DR   HSSP; P01810; 2FBJ.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    137       IG HEAVY CHAIN V REGION S43.
FT   DOMAIN       20     49       FRAMEWORK-1.
FT   DOMAIN       50     54       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       55     68       FRAMEWORK-2.
FT   DOMAIN       69     85       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       86    117       FRAMEWORK-3.
FT   DOMAIN      118    122       D SEGMENT.
FT   DOMAIN      123    137       JH2 SEGMENT.
FT   DISULFID     41    115       BY SIMILARITY.
FT   NON_TER     137    137
SQ   SEQUENCE   137 AA;  15200 MW;  ADD5881BF44B8EC9 CRC64;

  Query Match             52.9%;  Score 338.5;  DB 1;  Length 137;
  Best Local Similarity   55.3%;  Pred. No. 2.3e-28;
  Matches   68;  Conservative   20;  Mismatches   30;  Indels    5;  Gaps    2;

Qy          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60
              |||||| |||  |||:||::|||||| || :  ::|| | ||:||||:| | |  |   |
Db         20 QVQLQQPGAEFVKPGASVKLSCKASGYTFTSYLMHWVNQRPGRGLEWIGRIDPNSGGTTY 79

Qy         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHYGMDVWGRGTMVT 120
              :::|: :  :| |: :||| |:|||| |||:||||||| |       |  | ||:|| :|
Db         80 NEHFRSKATLTIDKPSSTAYMQLSSLTSEDSAVYYCARYR----LGRY-FDYWGQGTTLT 134

Qy        121 VSS 123
             |||
Db        135 VSS 137


Search completed: September  9, 2004, 11:06:52
Job time : 9.9359 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: September 9, 2004, 11:01:20 ; Search time 37.8462 Seconds
(without alignments)
1025.434 Million cell updates/sec

Title: US-09-880-748-2_COPY_1_123
Perfect score: 640
Sequence: 1 QVQLQQSGAEVKKPGSSVRV.....LFPHYGMDVWGRGTMVTVSS 123

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 70 summaries

Database : SPTREMBL_25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	456.5	71.3	116	4	Q9UL89	Q9ul89 homo sapien
2	439.5	68.7	159	4	Q96QS0	Q96qs0 homo sapien
3	403.5	63.0	124	4	Q9UL92	Q9ul92 homo sapien
4	391	61.1	614	4	Q96GA6	Q96ga6 homo sapien
5	390.5	61.0	496	4	Q96DK0	Q96dk0 homo sapien
6	388	60.6	125	4	Q9UL95	Q9ul95 homo sapien
7	386	60.3	119	4	Q9UL94	Q9ul94 homo sapien
8	386	60.3	119	5	Q9GYZ2	Q9gyz2 schistosoma
9	383.5	59.9	500	4	Q9BRV0	Q9brv0 homo sapien
10	373.5	58.4	145	11	Q924Q9	Q924q9 mus musculu
11	369.5	57.7	145	11	Q924Q6	Q924q6 mus musculu
12	368.5	57.6	613	11	Q8VCX7	Q8vcx7 mus musculu
13	368	57.5	146	11	Q924Q3	Q924q3 mus musculu
14	367	57.3	473	11	Q9D8L4	Q9d8l4 mus musculu
15	363	56.7	150	4	Q9Y298	Q9y298 homo sapien
16	362.5	56.6	463	11	Q99LC4	Q99lc4 mus musculu
17	361	56.4	497	4	Q8WY24	Q8wy24 homo sapien
18	360.5	56.3	145	11	Q924P7	Q924p7 mus musculu
19	360	56.2	117	11	Q9QXE9	Q9qxe9 mus musculu
20	359.5	56.2	143	11	Q924R0	Q924r0 mus musculu
21	359.5	56.2	145	11	Q924R4	Q924r4 mus musculu
22	357.5	55.9	143	11	Q924Q5	Q924q5 mus musculu
23	357	55.8	168	11	Q8VDC9	Q8vdc9 mus musculu
24	356.5	55.7	145	11	Q924R1	Q924r1 mus musculu
25	355.5	55.5	482	11	Q8K172	Q8k172 mus musculu
26	354.5	55.4	473	11	Q99L25	Q99125 mus musculu
27	354	55.3	146	11	Q924R8	Q924r8 mus musculu
28	353.5	55.2	143	11	Q924Q0	Q924q0 mus musculu
29	353.5	55.2	145	11	Q924R3	Q924r3 mus musculu
30	353.5	55.2	145	11	Q924Q7	Q924q7 mus musculu
31	352.5	55.1	118	11	Q9Z1C4	Q9z1c4 mus musculu
32	352.5	55.1	143	11	Q924R7	Q924r7 mus musculu
33	352	55.0	140	11	Q924R2	Q924r2 mus musculu
34	352	55.0	614	11	Q7TMT6	Q7tmt6 mus musculu
35	351.5	54.9	141	11	Q924Q4	Q924q4 mus musculu
36	351.5	54.9	143	11	Q91V67	Q91v67 mus musculu
37	351	54.8	142	11	Q924Q1	Q924q1 mus musculu
38	350.5	54.8	469	4	Q7Z7P5	Q7z7p5 homo sapien
39	350	54.7	117	11	Q9QXF0	Q9qxf0 mus musculu
40	348	54.4	140	11	Q924P8	Q924p8 mus musculu
41	347.5	54.3	143	11	Q91VA2	Q91va2 mus musculu
42	347	54.2	144	11	Q924P5	Q924p5 mus musculu
43	347	54.2	481	11	Q91WT1	Q91wt1 mus musculu
44	346.5	54.1	143	11	Q924P9	Q924p9 mus musculu
45	346.5	54.1	241	11	Q921A6	Q921a6 mus musculu
46	346	54.1	142	11	Q924Q2	Q924q2 mus musculu
47	344.5	53.8	137	11	Q924R6	Q924r6 mus musculu
48	344	53.8	468	11	Q99L31	Q99131 mus musculu
49	342.5	53.5	139	11	Q924R5	Q924r5 mus musculu
50	342.5	53.5	243	11	Q7TQM2	Q7tqm2 mus musculu
51	342	53.4	146	11	Q924Q8	Q924q8 mus musculu
52	342	53.4	147	11	Q925S3	Q925s3 mus musculu
53	342	53.4	480	11	Q8K0Z4	Q8k0z4 mus musculu
54	341	53.3	470	11	Q7TMK1	Q7tmk1 mus musculu
55	340	53.1	123	11	Q8VIJ1	Q8vij1 mus musculu
56	339	53.0	474	11	Q8R3H6	Q8r3h6 mus musculu
57	338	52.8	120	11	Q920E8	Q920e8 mus musculu
58	337.5	52.7	278	11	Q921K1	Q921k1 mus musculu
59	337.5	52.7	488	11	Q8K0F2	Q8k0f2 mus musculu
60	335	52.3	484	11	Q99LA6	Q99la6 mus musculu
61	331	51.7	157	4	O95978	O95978 homo sapien
62	331	51.7	489	11	Q8VCX4	Q8vcx4 mus musculu
63	330.5	51.6	109	11	Q9JL75	Q9jl75 mus musculu
64	328.5	51.3	488	11	Q91WR1	Q91wr1 mus musculu
65	326.5	51.0	110	11	Q9JL77	Q9jl77 mus musculu
66	324.5	50.7	143	11	Q924P6	Q924p6 mus musculu
67	322.5	50.4	110	11	Q9JL83	Q9jl83 mus musculu
68	322.5	50.4	136	11	Q7TPE3	Q7tpe3 mus musculu
69	320	50.0	481	11	Q91WT3	Q91wt3 mus musculu
70	319	49.8	111	11	Q9D9B8	Q9d9b8 mus musculu

ALIGNMENTS

RESULT 1
Q9UL89
ID Q9UL89 PRELIMINARY; PRT; 116 AA.
AC Q9UL89;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

```
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035025; AAD56261.1; -.
DR   HSSP; P01810; 2FBJ.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     116    116
SQ   SEQUENCE   116 AA;  12605 MW;  C8F9131DE13EA898 CRC64;

  Query Match             71.3%;  Score 456.5;  DB 4;  Length 116;
  Best Local Similarity   76.3%;  Pred. No. 1.1e-40;
  Matches   90;  Conservative   11;  Mismatches   14;  Indels    3;  Gaps    1;

Qy          6 QSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKYSQNFQ 65
              |||||||||||||:||||||||:: ||:|||||||||||||| |||: | | |:| ||
Db          2 QSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGRIIPILGIANYAQKFQ 61

Qy         66 GRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHYGMDVWGRGTMVTVSS 123
              ||| |||||:||||| |||||||||||||||| |      |:: |:|||||:|||||
Db         62 GRVTITADKSTSTAYMELSSLRSEDTAVYYCASSN---WGPYWYFDLWGRGTLVTVSS 116


RESULT 2
Q96QS0
ID   Q96QS0      PRELIMINARY;      PRT;   159 AA.
AC   Q96QS0;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Putative matrix cell adhesion molecule-3.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Tilson M.D.;
RT   "Homo sapiens putative microfibrillar protein with Ig-like domain 3
RT   mRNA (Matrix Cell Adhesion Molecule-3, Mat-CAM 3).";
RL   Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY039025; AAK82649.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
SQ   SEQUENCE   159 AA;  17497 MW;  5D29537E881FAF02 CRC64;

  Query Match             68.7%;  Score 439.5;  DB 4;  Length 159;
  Best Local Similarity   66.9%;  Pred. No. 1.1e-38;
  Matches   87;  Conservative   15;  Mismatches   21;  Indels    7;  Gaps    1;

Qy          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60
              |||| |||||||||:||:||||||| ||:|  :|||||||||| |||| | |  |:|:|
Db         20 QVQLVQSGAEVKKPGASVKVSCKASGYTFSNYYMNWVRQAPGQGPEWMGVINPSGGSARY 79

Qy         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLL-------FPHYGMDVW 113
              || ||||: :| | ||||  |:||||||:|||||:|||  ::         | :||||||
Db         80 SQKFQGRLTMTRDTSTSTVYMDLSSLRSDDTAVYFCAREMEITFGGAVSKGFYYYGMDVW 139

Qy        114 GRGTMVTVSS 123
              |:|| |||||
Db        140 GQGTTVTVSS 149


RESULT 3
Q9UL92
ID   Q9UL92      PRELIMINARY;      PRT;   124 AA.
AC   Q9UL92;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Myosin-reactive immunoglobulin heavy chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035022; AAD56258.1; -.
DR   HSSP; P01772; 2FB4.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     124    124
SQ   SEQUENCE   124 AA;  13580 MW;  1BAAACBD96ACD2A2 CRC64;

  Query Match             63.0%;  Score 403.5;  DB 4;  Length 124;
  Best Local Similarity   65.3%;  Pred. No. 5.2e-35;
  Matches   81;  Conservative   17;  Mismatches   25;  Indels    1;  Gaps    1;

Qy          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60
              :||| :|||||||||:||:||||||| ||::  ::|||||||||||||| | |  |:  |
Db          1 EVQLVESGAEVKKPGASVKVSCKASGYTFSSYYMHWVRQAPGQGLEWMGIINPSGGSTSY 60

Qy         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHYG-MDVWGRGTMV 119
              :| ||||| :| | ||||  |||||||||||||||||   :::   :   | ||:||:|
Db         61 AQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARGLYVVVPAAFSRFDYWGQGTLV 120

Qy        120 TVSS 123
              ||||
Db        121 TVSS 124


RESULT 4
Q96GA6
ID   Q96GA6      PRELIMINARY;      PRT;   614 AA.
AC   Q96GA6;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=B-cell;
RA   Strausberg R.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC009851; AAH09851.1; -.
DR   PIR; S15590; S15590.
DR   GO; GO:0005622; C:intracellular; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   InterPro; IPR000005; HTHAraC.
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DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 5.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS00041; HTH_ARAC_FAMILY_1; 1.
DR   PROSITE; PS50835; IG_LIKE; 5.
DR   PROSITE; PS00290; IG_MHC; 3.
KW   Hypothetical protein.
SQ   SEQUENCE   614 AA;  67921 MW;  55EF536E77AA9BBB CRC64;

  Query Match             61.1%;  Score 391;  DB 4;  Length 614;
  Best Local Similarity   62.8%;  Pred. No. 8e-33;
  Matches   81;  Conservative    9;  Mismatches   25;  Indels   14;  Gaps    2;

Qy          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60
              |:|| |||||||| ||||:||||||| ||    ::|||||||| ||||| | |  |    |
Db         20 QMQLVQSGAEVKKTGSSVKVSCKASGYTFTYRYLHWVRQAPGQALEWMGWITPFNGNTNY 79

Qy         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHY------GMDVWG 114
              :| || || || | | :|| ||||||||||||:|||||         |       |:||
Db         80 AQKFQDRVTITRDRSMNTAYMELSSLRSEDTAMYYCARG--------YSSSWDDAFDIWG 131

Qy        115 RGTMVTVSS 123
              :|||||||
Db        132 QGTMVTVSS 140


RESULT 5
Q96DK0
ID   Q96DK0      PRELIMINARY;      PRT;   496 AA.
AC   Q96DK0;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein FLJ25298.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Gastric mucosa;
RA   Ishibashi T., Kanehori K., Yosida M., Watanabe S., Ishida S., Ono Y.,
RA   Hotuta T., Hiraoka S., Murakawa K., Takiguchi S., Kusano J.,
RA   Watanabe M., Fujimori K., Tanai H., Ishida M., Yamashita H., Chiba Y.,
RA   Suzuki Y., Hata H., Nakagawa K., Mizuno S., Morinaga M., Kawamura M.,
RA   Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A.,
RA   Kawakami B., Nagai K., Isogai T., Sugano S.;
RT   "NEDO human cDNA sequencing project.";
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK058027; BAB71633.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   496 AA;  53532 MW;  C72EE1E247C86FED CRC64;

  Query Match             61.0%;  Score 390.5;  DB 4;  Length 496;
  Best Local Similarity   60.5%;  Pred. No. 6.9e-33;
  Matches   78;  Conservative   13;  Mismatches   27;  Indels   11;  Gaps    2;

Qy          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60
              || | ||||||:| |||||:||||||    | : |  ||||||||||:||||||| ||   |
Db         20 QVHLVQSGAELKMPGSSVKVSCKASANMFRSYAFTWVRQAPGQGLQWMGGIIPNFGAPNY 79

Qy         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHYG------MDVWG 114
              :|||| || |:||:||:|  |||:||  |||| ||| |        :||      :  ||
Db         80 AQNFQDRVTISADDSTTTVYMELTSLTFEDTAFYYCGRG-----LTYYGSGSYYYLQHWG 134

Qy        115 RGTMVTVSS 123
              :||:|||||
Db        135 QGTLVTVSS 143


RESULT 6
Q9UL95
ID   Q9UL95      PRELIMINARY;      PRT;   125 AA.
AC   Q9UL95;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Myosin-reactive immunoglobulin heavy chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035019; AAD56255.1; -.
DR   HSSP; P01810; 2FBJ.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER      1      1
FT   NON_TER    125    125
SQ   SEQUENCE   125 AA;  13516 MW;  0D3CD5C232488EAC CRC64;

  Query Match             60.6%;  Score 388;  DB 4;  Length 125;
  Best Local Similarity   63.2%;  Pred. No. 2.3e-33;
  Matches   79;  Conservative   14;  Mismatches   30;  Indels    2;  Gaps    1;

Qy          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60
              :||| :|||||||||:||:||||||| ||    ::|||||||||||||| | |  |    |
Db          1 EVQLVESGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWINPNSGGTNY 60

Qy         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSR--DLLLFPHYGMDVWGRGTM 118
              :|  |||| :| | : ||| |||| |||:||||||||||:    :       |:||:|||
Db         61 AQKVQGRVTMTRDTTISTAYMELSRLRSDDTAVYYCARSQGGGRIAAAGDAFDIWGQGTM 120

Qy        119 VTVSS 123
              |||||
Db        121 VTVSS 125


RESULT 7
Q9UL94
ID   Q9UL94      PRELIMINARY;      PRT;   119 AA.
AC   Q9UL94;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Myosin-reactive immunoglobulin heavy chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
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RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035020; AAD56256.1; -.
DR   HSSP; P01810; 2FBJ.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     119    119
SQ   SEQUENCE   119 AA;  13205 MW;  13E64F5345F4A16E CRC64;

  Query Match             60.3%;  Score 386;  DB 4;  Length 119;
  Best Local Similarity   64.2%;  Pred. No. 3.6e-33;
  Matches   79;  Conservative   13;  Mismatches   27;  Indels    4;  Gaps    1;

Qy          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60
              :||| :|||||||||:||:||||||| ||    ::||||||||||||| | |   | |
Db          1 EVQLVESGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWINPNSWTTNY 60

Qy         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHYGMDVWGRGTMVT 120
              :| |||:| :| | | ||| |||| |||:|||||||||     |:     | ||:||:||
Db         61 AQKFQGKVTMTKDTSISTAYMELSRLRSDDTAVYYCARGGGRGLW----FDPWGQGTLVT 116

Qy        121 VSS 123
              |||
Db        117 VSS 119


RESULT 8
Q9GYZ2
ID   Q9GYZ2      PRELIMINARY;      PRT;   119 AA.
AC   Q9GYZ2;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Monoclonal anti-idiotypic antibody NP30 heavy chain variable region
DE   (Fragment).
OS   Schistosoma japonicum (Blood fluke).
OC   Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC   Schistosomatoidea; Schistosomatidae; Schistosoma.
OX   NCBI_TaxID=6182;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Song X.T., Feng Z.Q., Guan X.H.;
RT   "Amplification, cloning and sequence analysis of the heavy chain
RT   variable region gene of monoclonal anti-idiotypic antibody NP30 of
RT   Schistosoma japonicum.";
RL   Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF282622; AAG01452.1; -.
DR   HSSP; P01772; 2FB4.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     119    119
SQ   SEQUENCE   119 AA;  13567 MW;  BA893873FD5FA6AB CRC64;

  Query Match             60.3%;  Score 386;  DB 5;  Length 119;
  Best Local Similarity   63.4%;  Pred. No. 3.6e-33;
  Matches   78;  Conservative   13;  Mismatches   28;  Indels    4;  Gaps    1;

Qy          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60
              |||| :|||||:|||:|||||||||| ||    :|||||||| ||||:| | |   |
Db          1 QVQLVESGAEVRKPGASVRVSCKASGYTFTGYYMNWVRQAPGHGLEWIGYINPSRGYTNY 60

Qy         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHYGMDVWGRGTMVT 120
              :| |: || :| |:| ||| |:| |||| |:|||||||  |      || :| ||:|| ||
Db         61 NQKFKDRVTMTTDKSFSTAYMDLRSLRSADSAVYYCARYYD----DHYCLDYWGQGTTVT 116

Qy        121 VSS 123
              |||
Db        117 VSS 119


RESULT 9
Q9BRV0
ID   Q9BRV0      PRELIMINARY;      PRT;   500 AA.
AC   Q9BRV0;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Prostate;
RA   Strausberg R.;
RL   Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC005951; AAH05951.1; -.
DR   HSSP; P01789; 1MCP.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   500 AA;  54154 MW;  0A9BF43F2A3CC6D9 CRC64;

  Query Match             59.9%;  Score 383.5;  DB 4;  Length 500;
  Best Local Similarity   60.3%;  Pred. No. 3.9e-32;
  Matches   79;  Conservative   12;  Mismatches   29;  Indels   11;  Gaps    2;

Qy          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60
              || | ||||||  ||:||||||| ||  |:  :| |||||||||||||| | |     ::
Db         20 QVHLVQSGAEVMSPGASVRVSCKTSGYAFHTYSIIWVRQAPGQGLEWMGWISPSSDNTRF 79

Qy         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCAR--------SRDLLLFPHYGMDV 112
              :: ||||| :| | ||||  ||| ||||:|||||||||          |   : :| |||
Db         80 AKKFQGRVTLTTDTSTSTVYMELRSLRSDDTAVYYCARRYCSYSSCQND---YYYYYMDV 136

Qy        113 WGRGTMVTVSS 123
              ||:|| |||||
Db        137 WGKGTTVTVSS 147


RESULT 10
Q924Q9
ID   Q924Q9      PRELIMINARY;      PRT;   145 AA.
AC   Q924Q9;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   VH186.2-D-J-C mu protein (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RA   Kozono Y., Kozono H., Azuma T.;
RT   "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT   Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT   Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB067791; BAB63276.1; -.
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DR   PIR; F28833; F28833.
DR   PIR; F33932; F33932.
DR   PIR; PH1105; PH1105.
DR   PIR; PH1108; PH1108.
DR   PIR; PH1114; PH1114.
DR   PIR; PH1118; PH1118.
DR   PIR; PH1119; PH1119.
DR   PIR; PH1125; PH1125.
DR   PIR; PH1126; PH1126.
DR   PIR; PH1128; PH1128.
DR   PIR; PH1129; PH1129.
DR   PIR; PH1131; PH1131.
DR   PIR; PH1134; PH1134.
DR   PIR; PH1137; PH1137.
DR   PIR; PH1139; PH1139.
DR   PIR; PH1142; PH1142.
DR   PIR; PH1144; PH1144.
DR   PIR; PH1147; PH1147.
DR   PIR; PH1149; PH1149.
DR   PIR; PH1150; PH1150.
DR   PIR; PH1151; PH1151.
DR   PIR; PH1152; PH1152.
DR   PIR; PH1153; PH1153.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     145    145
SQ   SEQUENCE   145 AA;  16001 MW;  0F409EB09FA333D2 CRC64;

  Query Match             58.4%;  Score 373.5;  DB 11;  Length 145;
  Best Local Similarity   58.5%;  Pred. No. 9.8e-32;
  Matches   72;  Conservative   22;  Mismatches   26;  Indels    3;  Gaps    1;

Qy          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60
              |||||| |||: |||:||::|||||| || :  ::||:| ||:||||:| | |   |  ||
Db          1 QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGRGLEWIGRIDPNSGGTKY 60

Qy         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHYGMDVWGRGTMVT 120
              :: |: :  :| |: :||| |:|||| |||:|||||||    |:  :| || ||:|| ||
Db         61 NEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYYCARS---LITTYYAMDYWGQGTSVT 117

Qy        121 VSS 123
              |||
Db        118 VSS 120


RESULT 11
Q924Q6
ID   Q924Q6      PRELIMINARY;      PRT;   145 AA.
AC   Q924Q6;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   VH186.2-D-J-C mu protein (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RA   Kozono Y., Kozono H., Azuma T.;
RT   "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT   Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT   Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB067794; BAB63279.1; -.
DR   PIR; F28833; F28833.
DR   PIR; F33932; F33932.
DR   PIR; PH1105; PH1105.
DR   PIR; PH1108; PH1108.
DR   PIR; PH1114; PH1114.
DR   PIR; PH1118; PH1118.
DR   PIR; PH1119; PH1119.
DR   PIR; PH1125; PH1125.
DR   PIR; PH1126; PH1126.
DR   PIR; PH1128; PH1128.
DR   PIR; PH1129; PH1129.
DR   PIR; PH1131; PH1131.
DR   PIR; PH1134; PH1134.
DR   PIR; PH1137; PH1137.
DR   PIR; PH1139; PH1139.
DR   PIR; PH1142; PH1142.
DR   PIR; PH1144; PH1144.
DR   PIR; PH1147; PH1147.
DR   PIR; PH1149; PH1149.
DR   PIR; PH1150; PH1150.
DR   PIR; PH1151; PH1151.
DR   PIR; PH1152; PH1152.
DR   PIR; PH1153; PH1153.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     145    145
SQ   SEQUENCE   145 AA;  16011 MW;  9BC0846D40DF97EA CRC64;

  Query Match             57.7%;  Score 369.5;  DB 11;  Length 145;
  Best Local Similarity   58.5%;  Pred. No. 2.6e-31;
  Matches   72;  Conservative   21;  Mismatches   27;  Indels    3;  Gaps    1;

Qy          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60
              |||||| |||: |||:||::|||||| || :  ::||:| ||:||||:| | |   |  ||
Db          1 QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGRGLEWIGRIDPNSGGTKY 60

Qy         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHYGMDVWGRGTMVT 120
              :: |: :  :| |: :||| |:|||| |||:|||||||    |:  :| || ||:|| ||
Db         61 NEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYYCARS---TLSHYYAMDYWGQGTSVT 117

Qy        121 VSS 123
              |||
Db        118 VSS 120


RESULT 12
Q8VCX7
ID   Q8VCX7      PRELIMINARY;      PRT;   613 AA.
AC   Q8VCX7;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
GN   IGH-6.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Salivary gland;
RA   Strausberg R.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC018315; AAH18315.1; -.
DR   MGD; MGI:96448; Igh-6.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 5.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 5.
DR   PROSITE; PS00290; IG_MHC; 3.
```

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KW   Hypothetical protein.
SQ   SEQUENCE   613 AA;  67855 MW;  41A9384DD4C22862 CRC64;

  Query Match             57.6%;  Score 368.5;  DB 11;  Length 613;
  Best Local Similarity   58.5%;  Pred. No. 2e-30;
  Matches   72;  Conservative   19;  Mismatches   27;  Indels    5;  Gaps    1;

Qy          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60
              |||||||||||: |||:||::||||:| ||::  | ||:| || ||||:| |:|  |:  |
Db         20 QVQLQQSGAELMKPGASVKISCKATGYTFSSYWIEWVKQRPGHGLEWIGEILPGSGSTNY 79

Qy         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHYGMDVWGRGTMVT 120
              :: |:|:   ||| |::|| |:|||| |||:|||||||      |     |||| || ||
Db         80 NEKFKGKATFTADTSSNTAYMQLSSLTSEDSAVYYCARRLGRWYF-----DVWGAGTTVT 134

Qy        121 VSS 123
              |||
Db        135 VSS 137
```

```
RESULT 13
Q924Q3
ID   Q924Q3      PRELIMINARY;      PRT;   146 AA.
AC   Q924Q3;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   VH186.2-D-J-C mu protein (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RA   Kozono Y., Kozono H., Azuma T.;
RT   "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT   Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT   Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB067797; BAB63282.1; -.
DR   PIR; F28833; F28833.
DR   PIR; F33932; F33932.
DR   PIR; PH1105; PH1105.
DR   PIR; PH1108; PH1108.
DR   PIR; PH1114; PH1114.
DR   PIR; PH1118; PH1118.
DR   PIR; PH1119; PH1119.
DR   PIR; PH1125; PH1125.
DR   PIR; PH1126; PH1126.
DR   PIR; PH1128; PH1128.
DR   PIR; PH1129; PH1129.
DR   PIR; PH1131; PH1131.
DR   PIR; PH1134; PH1134.
DR   PIR; PH1137; PH1137.
DR   PIR; PH1139; PH1139.
DR   PIR; PH1142; PH1142.
DR   PIR; PH1144; PH1144.
DR   PIR; PH1147; PH1147.
DR   PIR; PH1149; PH1149.
DR   PIR; PH1150; PH1150.
DR   PIR; PH1151; PH1151.
DR   PIR; PH1152; PH1152.
DR   PIR; PH1153; PH1153.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1       1
FT   NON_TER     146     146
SQ   SEQUENCE   146 AA;  16136 MW;  CEA8DD6E1955807F CRC64;
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```
  Query Match             57.5%;  Score 368;  DB 11;  Length 146;
  Best Local Similarity   58.5%;  Pred. No. 3.8e-31;
  Matches   72;  Conservative   21;  Mismatches   28;  Indels    2;  Gaps    1;

Qy          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60
              |||||| |||: |||:||::|||||| || :  ::||:| ||:||||:| | |  |  ||
Db          1 QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGRGLEWIGRIDPNSGGTKY 60

Qy         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHYGMDVWGRGTMVT 120
              :: |: :  :| |: :||| |:|||| |||:|||||||  |  :  | || ||:|| ||
Db         61 NEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYYCARS--LYDYGDYAMDYWGQGTSVT 118

Qy        121 VSS 123
              |||
Db        119 VSS 121
```

```
RESULT 14
Q9D8L4
ID   Q9D8L4      PRELIMINARY;      PRT;   473 AA.
AC   Q9D8L4;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   1810060O09Rik protein.
GN   IGH-1 OR 1810060O09RIK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Pancreas;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
DR   EMBL; AK007918; BAB25349.1; -.
DR   PIR; S26746; S26746.
DR   HSSP; P01842; 7FAB.
DR   MGD; MGI:96443; Igh-1.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 1.
SQ   SEQUENCE   473 AA;  51699 MW;  9DED57A514475FBB CRC64;

  Query Match             57.3%;  Score 367;  DB 11;  Length 473;
  Best Local Similarity   57.9%;  Pred. No. 2.1e-30;
  Matches   73;  Conservative   22;  Mismatches   21;  Indels   10;  Gaps    2;

Qy          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60
              ||||:|||||: |||:||::|||||| || :  ||||:| |||||||:| | |  |:  |
```

```
Db         20 QVQLKQSGAELVKPGASVKISCKASGYTFTDYYINWVKQRPGQGLEWIGKIGPGSGSTYY 79

Qy         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHYGMD---VWGRGT 117
              :: |:|:  :|||:|:||| |:|||| |||:|||:|||| |  |    ||:||
Db         80 NEKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYFCARS-------GYDYDWFAYWGQGT 132

Qy        118 MVTVSS 123
              :||||:
Db        133 LVTVSA 138


RESULT 15
Q9Y298
ID   Q9Y298      PRELIMINARY;      PRT;   150 AA.
AC   Q9Y298;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   IgG VH protein precursor (Fragment).
GN   IGG VH.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98322155; PubMed=9657749;
RA   Jacquemin M.G., Vander Elst L.P.L.;
RT   "Mechanism and kinetics of factor VIII inactivation: study with an
RT   IgG4 monclonal antibody derived from a hemophilia A patient with
RT   inhibitor.";
RL   Blood 92:496-506(1998).
DR   EMBL; AJ224083; CAA11829.1; -.
DR   HSSP; P01772; 2FB4.
DR   GO; GO:0005887; C:integral to plasma membrane; NAS.
DR   GO; GO:0016489; F:immunoglobulin receptor activity; NAS.
DR   GO; GO:0016066; P:cellular defense response (sensu Vertebrata); NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Signal.
FT   SIGNAL        1     19       POTENTIAL.
FT   NON_TER     150    150
SQ   SEQUENCE   150 AA;  16031 MW;  563D164AB22802D5 CRC64;

  Query Match             56.7%;  Score 363;  DB 4;  Length 150;
  Best Local Similarity   60.2%;  Pred. No. 1.3e-30;
  Matches   74;  Conservative   14;  Mismatches   29;  Indels    6;  Gaps    1;

Qy          1 QVQLQQSGAEVKKPGSSVRVSCKASGGTFNNNAINWVRQAPGQGLEWMGGIIPMFGTAKY 60
              |||| |||||||||:||:|||| || |     ::|| ||||:||||:|   |  | : |
Db         20 QVQLVQSGAEVKKPGASVKVSCKVSGYTLTELPVHWVGQAPGKGLEWVGSFDPESGESIY 79

Qy         61 SQNFQGRVAITADESTSTASMELSSLRSEDTAVYYCARSRDLLLFPHYGMDVWGRGTMVT 120
              :: ||| | :||| ||  | ||||||||:||||||||      :      |:||:|||||
Db         80 AREFQGSVTMTADTSTDIAYMELSSLRSDDTAVYYCA------VPDPDAFDIWGQGTMVT 133

Qy        121 VSS 123
              |||
Db        134 VSS 136


Search completed: September  9, 2004, 11:08:43
Job time : 39.8462 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: September 9, 2004, 10:53:58 ; Search time 47.9103 Seconds
(without alignments)
654.615 Million cell updates/sec

Title: US-09-880-748-2_COPY_139_249
Perfect score: 585
Sequence: 1 AFSSELTQDPAVSVALGQTV.....RDSSGNHWVFGGGTELTVLG 111

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 70 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	585	100.0	248	5	ABP44336	Abp44336 Human BLy
2	585	100.0	248	5	ABP44586	Abp44586 Human BLy
3	585	100.0	248	5	ABP44343	Abp44343 Human BLy
4	585	100.0	248	5	ABP44328	Abp44328 Human BLy
5	585	100.0	248	5	ABP44612	Abp44612 Human BLy
6	585	100.0	249	5	ABP44344	Abp44344 Human BLy
7	585	100.0	249	5	ABP44348	Abp44348 Human BLy
8	585	100.0	249	5	ABP44350	Abp44350 Human BLy
9	585	100.0	249	5	ABP44432	Abp44432 Human BLy
10	585	100.0	249	5	ABP44451	Abp44451 Human BLy
11	585	100.0	249	5	ABP44477	Abp44477 Human BLy
12	585	100.0	249	5	ABP44497	Abp44497 Human BLy
13	585	100.0	249	5	ABP44548	Abp44548 Human BLy
14	585	100.0	249	5	ABP44613	Abp44613 Human BLy
15	585	100.0	249	5	ABP44621	Abp44621 Human BLy
16	585	100.0	249	5	ABP44644	Abp44644 Human BLy
17	585	100.0	249	5	ABP44660	Abp44660 Human BLy
18	585	100.0	249	5	ABP44664	Abp44664 Human BLy
19	585	100.0	249	5	ABP44701	Abp44701 Human BLy
20	585	100.0	249	5	ABP44710	Abp44710 Human BLy
21	585	100.0	249	5	ABP44732	Abp44732 Human BLy
22	585	100.0	249	5	ABP44747	Abp44747 Human BLy
23	585	100.0	249	5	ABP44756	Abp44756 Human BLy
24	585	100.0	249	5	ABP44760	Abp44760 Human BLy
25	585	100.0	249	5	ABP43991	Abp43991 Human BLy
26	585	100.0	249	5	ABP44321	Abp44321 Human BLy
27	585	100.0	249	5	ABP44327	Abp44327 Human BLy
28	585	100.0	249	5	ABP44333	Abp44333 Human BLy
29	585	100.0	249	5	ABP44374	Abp44374 Human BLy
30	585	100.0	249	5	ABP44387	Abp44387 Human BLy
31	585	100.0	249	5	ABP44401	Abp44401 Human BLy
32	585	100.0	249	5	ABP44452	Abp44452 Human BLy
33	585	100.0	249	5	ABP44487	Abp44487 Human BLy
34	585	100.0	249	5	ABP44493	Abp44493 Human BLy
35	585	100.0	249	5	ABP44506	Abp44506 Human BLy
36	585	100.0	249	5	ABP44509	Abp44509 Human BLy
37	585	100.0	249	5	ABP44526	Abp44526 Human BLy
38	585	100.0	249	5	ABP44553	Abp44553 Human BLy
39	585	100.0	249	5	ABP44652	Abp44652 Human BLy
40	585	100.0	249	5	ABP44662	Abp44662 Human BLy
41	585	100.0	249	5	ABP44685	Abp44685 Human BLy
42	585	100.0	249	5	ABP44722	Abp44722 Human BLy
43	585	100.0	249	5	ABP44770	Abp44770 Human BLy
44	585	100.0	249	5	ABP44794	Abp44794 Human BLy
45	585	100.0	249	5	ABP44810	Abp44810 Human BLy
46	585	100.0	249	5	ABP44376	Abp44376 Human BLy
47	585	100.0	249	5	ABP44389	Abp44389 Human BLy
48	585	100.0	249	5	ABP44393	Abp44393 Human BLy
49	585	100.0	249	5	ABP44397	Abp44397 Human BLy
50	585	100.0	249	5	ABP44411	Abp44411 Human BLy
51	585	100.0	249	5	ABP44448	Abp44448 Human BLy
52	585	100.0	249	5	ABP44457	Abp44457 Human BLy
53	585	100.0	249	5	ABP44463	Abp44463 Human BLy
54	585	100.0	249	5	ABP44488	Abp44488 Human BLy
55	585	100.0	249	5	ABP44505	Abp44505 Human BLy
56	585	100.0	249	5	ABP44561	Abp44561 Human BLy
57	585	100.0	249	5	ABP44596	Abp44596 Human BLy
58	585	100.0	249	5	ABP44603	Abp44603 Human BLy
59	585	100.0	249	5	ABP44636	Abp44636 Human BLy
60	585	100.0	249	5	ABP44647	Abp44647 Human BLy
61	585	100.0	249	5	ABP44705	Abp44705 Human BLy
62	585	100.0	249	5	ABP44724	Abp44724 Human BLy
63	585	100.0	249	5	ABP44740	Abp44740 Human BLy
64	585	100.0	249	5	ABP44743	Abp44743 Human BLy
65	585	100.0	249	5	ABP44753	Abp44753 Human BLy
66	585	100.0	249	5	ABP44765	Abp44765 Human BLy
67	585	100.0	249	5	ABP44346	Abp44346 Human BLy
68	585	100.0	249	5	ABP44388	Abp44388 Human BLy
69	585	100.0	249	5	ABP44398	Abp44398 Human BLy
70	585	100.0	249	5	ABP44422	Abp44422 Human BLy

ALIGNMENTS

RESULT 1
ABP44336
ID ABP44336 standard; protein; 248 AA.
XX
AC ABP44336;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human BLyS binding scFv SEQ ID 347.
XX
KW BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS Homo sapiens.
XX
PN WO200202641-A1.
XX
PD 10-JAN-2002.
XX

PF 15-JUN-2001; 2001WO-US019110.
XX
PR 16-JUN-2000; 2000US-0212210P.
PR 17-OCT-2000; 2000US-0240816P.
PR 16-MAR-2001; 2001US-0276248P.
PR 21-MAR-2001; 2001US-0277379P.
PR 25-MAY-2001; 2001US-0293499P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX
DR WPI; 2002-114799/15.
XX
PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
PT diagnosis and treatment of cancers and immune disorders.
XX
PS Claim 1; Page 818-819; 3148pp; English.

CC This invention describes novel antibodies that immunospecifically bind to
CC B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of BLyS. The antibodies bind to BLyS
CC and so may be used to detect and quantitate the presence of BLyS in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of BLyS. They may also be
CC administered to treat diseases associated with aberrant BLyS expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention
XX
SQ Sequence 248 AA;

Query Match 100.0%; Score 585; DB 5; Length 248;
Best Local Similarity 100.0%; Pred. No. 1e-36;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 AFSSELTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        138 AFSSELTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIP 197

Qy         61 DRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 111
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        198 DRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 248
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RESULT 2
ABP44586
ID ABP44586 standard; protein; 248 AA.
XX
AC ABP44586;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human BLyS binding scFv SEQ ID 597.
XX
KW BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS Homo sapiens.
XX
PN WO200202641-A1.
XX
PD 10-JAN-2002.
XX
PF 15-JUN-2001; 2001WO-US019110.
XX
PR 16-JUN-2000; 2000US-0212210P.
PR 17-OCT-2000; 2000US-0240816P.
PR 16-MAR-2001; 2001US-0276248P.
PR 21-MAR-2001; 2001US-0277379P.
PR 25-MAY-2001; 2001US-0293499P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX
DR WPI; 2002-114799/15.
XX
PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
PT diagnosis and treatment of cancers and immune disorders.
XX
PS Claim 1; Page 1114-1115; 3148pp; English.
XX
CC This invention describes novel antibodies that immunospecifically bind to
CC B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of BLyS. The antibodies bind to BLyS
CC and so may be used to detect and quantitate the presence of BLyS in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of BLyS. They may also be
CC administered to treat diseases associated with aberrant BLyS expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention
XX
SQ Sequence 248 AA;

Query Match 100.0%; Score 585; DB 5; Length 248;
Best Local Similarity 100.0%; Pred. No. 1e-36;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 AFSSELTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        138 AFSSELTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIP 197

Qy         61 DRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 111
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        198 DRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 248
```

RESULT 3
ABP44343
ID ABP44343 standard; protein; 248 AA.
XX
AC ABP44343;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human BLyS binding scFv SEQ ID 354.
XX
KW BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.
XX

OS Homo sapiens.
XX
PN WO200202641-A1.
XX
PD 10-JAN-2002.
XX
PF 15-JUN-2001; 2001WO-US019110.
XX
PR 16-JUN-2000; 2000US-0212210P.
PR 17-OCT-2000; 2000US-0240816P.
PR 16-MAR-2001; 2001US-0276248P.
PR 21-MAR-2001; 2001US-0277379P.
PR 25-MAY-2001; 2001US-0293499P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX
DR WPI; 2002-114799/15.
XX
PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
PT diagnosis and treatment of cancers and immune disorders.
XX
PS Claim 1; Page 826-827; 3148pp; English.
XX
CC This invention describes novel antibodies that immunospecifically bind to
CC B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of BLyS. The antibodies bind to BLyS
CC and so may be used to detect and quantitate the presence of BLyS in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of BLyS. They may also be
CC administered to treat diseases associated with aberrant BLyS expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention
XX
SQ Sequence 248 AA;

Query Match 100.0%; Score 585; DB 5; Length 248;
Best Local Similarity 100.0%; Pred. No. 1e-36;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 AFSSELTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        138 AFSSELTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIP 197

Qy         61 DRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 111
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        198 DRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 248
```

RESULT 4
ABP44328
ID ABP44328 standard; protein; 248 AA.
XX
AC ABP44328;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human BLyS binding scFv SEQ ID 339.
XX
KW BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS Homo sapiens.
XX
PN WO200202641-A1.
XX
PD 10-JAN-2002.
XX
PF 15-JUN-2001; 2001WO-US019110.
XX
PR 16-JUN-2000; 2000US-0212210P.
PR 17-OCT-2000; 2000US-0240816P.
PR 16-MAR-2001; 2001US-0276248P.
PR 21-MAR-2001; 2001US-0277379P.
PR 25-MAY-2001; 2001US-0293499P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX
DR WPI; 2002-114799/15.
XX
PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
PT diagnosis and treatment of cancers and immune disorders.
XX
PS Claim 1; Page 808-809; 3148pp; English.
XX
CC This invention describes novel antibodies that immunospecifically bind to
CC B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of BLyS. The antibodies bind to BLyS
CC and so may be used to detect and quantitate the presence of BLyS in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of BLyS. They may also be
CC administered to treat diseases associated with aberrant BLyS expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention
XX
SQ Sequence 248 AA;

Query Match 100.0%; Score 585; DB 5; Length 248;
Best Local Similarity 100.0%; Pred. No. 1e-36;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 AFSSELTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        138 AFSSELTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIP 197

Qy         61 DRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 111
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        198 DRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 248
```

RESULT 5
ABP44612
ID ABP44612 standard; protein; 248 AA.
XX
AC ABP44612;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human BLyS binding scFv SEQ ID 623.
XX
KW BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;

KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS Homo sapiens.
XX
PN WO200202641-A1.
XX
PD 10-JAN-2002.
XX
PF 15-JUN-2001; 2001WO-US019110.
XX
PR 16-JUN-2000; 2000US-0212210P.
PR 17-OCT-2000; 2000US-0240816P.
PR 16-MAR-2001; 2001US-0276248P.
PR 21-MAR-2001; 2001US-0277379P.
PR 25-MAY-2001; 2001US-0293499P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX
DR WPI; 2002-114799/15.
XX
PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
PT diagnosis and treatment of cancers and immune disorders.
XX
PS Claim 1; Page 1145-1146; 3148pp; English.
XX
CC This invention describes novel antibodies that immunospecifically bind to
CC B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of BLyS. The antibodies bind to BLyS
CC and so may be used to detect and quantitate the presence of BLyS in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of BLyS. They may also be
CC administered to treat diseases associated with aberrant BLyS expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention
XX
SQ Sequence 248 AA;

Query Match 100.0%; Score 585; DB 5; Length 248;
Best Local Similarity 100.0%; Pred. No. 1e-36;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AFSSELTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIP 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 138 AFSSELTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIP 197

Qy 61 DRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 111
|||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 198 DRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 248

RESULT 6
ABP44344
ID ABP44344 standard; protein; 249 AA.
XX
AC ABP44344;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human BLyS binding scFv SEQ ID 355.
XX
KW BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS Homo sapiens.
XX
PN WO200202641-A1.
XX
PD 10-JAN-2002.
XX
PF 15-JUN-2001; 2001WO-US019110.
XX
PR 16-JUN-2000; 2000US-0212210P.
PR 17-OCT-2000; 2000US-0240816P.
PR 16-MAR-2001; 2001US-0276248P.
PR 21-MAR-2001; 2001US-0277379P.
PR 25-MAY-2001; 2001US-0293499P.
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PA (HUMA-) HUMAN GENOME SCI INC.
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PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX
DR WPI; 2002-114799/15.
XX
PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
PT diagnosis and treatment of cancers and immune disorders.
XX
PS Claim 1; Page 827-828; 3148pp; English.
XX
CC This invention describes novel antibodies that immunospecifically bind to
CC B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of BLyS. The antibodies bind to BLyS
CC and so may be used to detect and quantitate the presence of BLyS in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of BLyS. They may also be
CC administered to treat diseases associated with aberrant BLyS expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention
XX
SQ Sequence 249 AA;

Query Match 100.0%; Score 585; DB 5; Length 249;
Best Local Similarity 100.0%; Pred. No. 1e-36;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AFSSELTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIP 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 139 AFSSELTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIP 198

Qy 61 DRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 111
|||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 199 DRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 249

RESULT 7
ABP44348
ID ABP44348 standard; protein; 249 AA.
XX
AC ABP44348;

XX
DT 19-AUG-2002 (first entry)
XX
DE Human BLyS binding scFv SEQ ID 359.
XX
KW BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS Homo sapiens.
XX
PN WO200202641-A1.
XX
PD 10-JAN-2002.
XX
PF 15-JUN-2001; 2001WO-US019110.
XX
PR 16-JUN-2000; 2000US-0212210P.
PR 17-OCT-2000; 2000US-0240816P.
PR 16-MAR-2001; 2001US-0276248P.
PR 21-MAR-2001; 2001US-0277379P.
PR 25-MAY-2001; 2001US-0293499P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX
DR WPI; 2002-114799/15.
XX
PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
PT diagnosis and treatment of cancers and immune disorders.
XX
PS Claim 1; Page 832-833; 3148pp; English.
XX
CC This invention describes novel antibodies that immunospecifically bind to
CC B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of BLyS. The antibodies bind to BLyS
CC and so may be used to detect and quantitate the presence of BLyS in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of BLyS. They may also be
CC administered to treat diseases associated with aberrant BLyS expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention
XX
SQ Sequence 249 AA;

Query Match 100.0%; Score 585; DB 5; Length 249;
Best Local Similarity 100.0%; Pred. No. 1e-36;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AFSSELTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIP 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 139 AFSSELTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIP 198

Qy 61 DRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 111
||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 199 DRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 249

RESULT 8
ABP44350

ID ABP44350 standard; protein; 249 AA.
XX
AC ABP44350;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human BLyS binding scFv SEQ ID 361.
XX
KW BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS Homo sapiens.
XX
PN WO200202641-A1.
XX
PD 10-JAN-2002.
XX
PF 15-JUN-2001; 2001WO-US019110.
XX
PR 16-JUN-2000; 2000US-0212210P.
PR 17-OCT-2000; 2000US-0240816P.
PR 16-MAR-2001; 2001US-0276248P.
PR 21-MAR-2001; 2001US-0277379P.
PR 25-MAY-2001; 2001US-0293499P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX
DR WPI; 2002-114799/15.
XX
PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
PT diagnosis and treatment of cancers and immune disorders.
XX
PS Claim 1; Page 834-835; 3148pp; English.
XX
CC This invention describes novel antibodies that immunospecifically bind to
CC B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of BLyS. The antibodies bind to BLyS
CC and so may be used to detect and quantitate the presence of BLyS in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of BLyS. They may also be
CC administered to treat diseases associated with aberrant BLyS expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention
XX
SQ Sequence 249 AA;

Query Match 100.0%; Score 585; DB 5; Length 249;
Best Local Similarity 100.0%; Pred. No. 1e-36;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AFSSELTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIP 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 139 AFSSELTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIP 198

Qy 61 DRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 111
||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 199 DRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 249

```
RESULT 9
ABP44432
ID   ABP44432 standard; protein; 249 AA.
XX
AC   ABP44432;
XX
DT   19-AUG-2002  (first entry)
XX
DE   Human BLyS binding scFv SEQ ID 443.
XX
KW   BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW   tumour necrosis factor; B cell proliferation; B cell differentiation;
KW   immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW   antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW   systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW   common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS   Homo sapiens.
XX
PN   WO200202641-A1.
XX
PD   10-JAN-2002.
XX
PF   15-JUN-2001; 2001WO-US019110.
XX
PR   16-JUN-2000; 2000US-0212210P.
PR   17-OCT-2000; 2000US-0240816P.
PR   16-MAR-2001; 2001US-0276248P.
PR   21-MAR-2001; 2001US-0277379P.
PR   25-MAY-2001; 2001US-0293499P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
PA   (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI   Ruben SM,  Barash SC,  Choi GH,  Vaughan T,  Hilbert D;
XX
DR   WPI; 2002-114799/15.
XX
PT   Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
PT   diagnosis and treatment of cancers and immune disorders.
XX
PS   Claim 1; Page 932-933; 3148pp; English.
XX
CC   This invention describes novel antibodies that immunospecifically bind to
CC   B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the
CC   tumour necrosis factor (TNF) super family and induces B cell
CC   proliferation and differentiation. The antibodies of the invention have
CC   cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC   antirheumatic and antiAIDS activity and can be used in vaccines to
CC   inhibit the expression and activity of BLyS. The antibodies bind to BLyS
CC   and so may be used to detect and quantitate the presence of BLyS in
CC   biological samples and may be used in this way to diagnose disease
CC   associated with aberrant expression of BLyS. They may also be
CC   administered to treat diseases associated with aberrant BLyS expression
CC   and activity such as cancer, immune, and autoimmune disorders and
CC   diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC   immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC   acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC   the antibodies and fragments of the antibodies described in the method of
CC   the invention
XX
SQ   Sequence 249 AA;

  Query Match             100.0%;  Score 585;  DB 5;  Length 249;
  Best Local Similarity   100.0%;  Pred. No. 1e-36;
  Matches  111;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AFSSELTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 AFSSELTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIP 198

Qy         61 DRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 111
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        199 DRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 249

RESULT 10
ABP44451
ID   ABP44451 standard; protein; 249 AA.
XX
AC   ABP44451;
XX
DT   19-AUG-2002  (first entry)
XX
DE   Human BLyS binding scFv SEQ ID 462.
XX
KW   BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW   tumour necrosis factor; B cell proliferation; B cell differentiation;
KW   immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW   antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW   systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW   common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS   Homo sapiens.
XX
PN   WO200202641-A1.
XX
PD   10-JAN-2002.
XX
PF   15-JUN-2001; 2001WO-US019110.
XX
PR   16-JUN-2000; 2000US-0212210P.
PR   17-OCT-2000; 2000US-0240816P.
PR   16-MAR-2001; 2001US-0276248P.
PR   21-MAR-2001; 2001US-0277379P.
PR   25-MAY-2001; 2001US-0293499P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
PA   (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI   Ruben SM,  Barash SC,  Choi GH,  Vaughan T,  Hilbert D;
XX
DR   WPI; 2002-114799/15.
XX
PT   Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
PT   diagnosis and treatment of cancers and immune disorders.
XX
PS   Claim 1; Page 954-955; 3148pp; English.
XX
CC   This invention describes novel antibodies that immunospecifically bind to
CC   B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the
CC   tumour necrosis factor (TNF) super family and induces B cell
CC   proliferation and differentiation. The antibodies of the invention have
CC   cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC   antirheumatic and antiAIDS activity and can be used in vaccines to
CC   inhibit the expression and activity of BLyS. The antibodies bind to BLyS
CC   and so may be used to detect and quantitate the presence of BLyS in
CC   biological samples and may be used in this way to diagnose disease
CC   associated with aberrant expression of BLyS. They may also be
CC   administered to treat diseases associated with aberrant BLyS expression
CC   and activity such as cancer, immune, and autoimmune disorders and
CC   diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC   immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC   acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC   the antibodies and fragments of the antibodies described in the method of
CC   the invention
XX
SQ   Sequence 249 AA;

  Query Match             100.0%;  Score 585;  DB 5;  Length 249;
  Best Local Similarity   100.0%;  Pred. No. 1e-36;
  Matches  111;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AFSSELTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        139 AFSSELTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIP 198

Qy         61 DRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 111
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        199 DRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 249


RESULT 11
ABP44477
ID   ABP44477 standard; protein; 249 AA.
XX
AC   ABP44477;
XX
DT   19-AUG-2002  (first entry)
XX
DE   Human BLyS binding scFv SEQ ID 488.
XX
KW   BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW   tumour necrosis factor; B cell proliferation; B cell differentiation;
KW   immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW   antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW   systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW   common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS   Homo sapiens.
XX
PN   WO200202641-A1.
XX
PD   10-JAN-2002.
XX
PF   15-JUN-2001; 2001WO-US019110.
XX
PR   16-JUN-2000; 2000US-0212210P.
PR   17-OCT-2000; 2000US-0240816P.
PR   16-MAR-2001; 2001US-0276248P.
PR   21-MAR-2001; 2001US-0277379P.
PR   25-MAY-2001; 2001US-0293499P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
PA   (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI   Ruben SM,  Barash SC,  Choi GH,  Vaughan T,  Hilbert D;
XX
DR   WPI; 2002-114799/15.
XX
PT   Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
PT   diagnosis and treatment of cancers and immune disorders.
XX
PS   Claim 1; Page 985-986; 3148pp; English.
XX
CC   This invention describes novel antibodies that immunospecifically bind to
CC   B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the
CC   tumour necrosis factor (TNF) super family and induces B cell
CC   proliferation and differentiation. The antibodies of the invention have
CC   cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC   antirheumatic and antiAIDS activity and can be used in vaccines to
CC   inhibit the expression and activity of BLyS. The antibodies bind to BLyS
CC   and so may be used to detect and quantitate the presence of BLyS in
CC   biological samples and may be used in this way to diagnose disease
CC   associated with aberrant expression of BLyS. They may also be
CC   administered to treat diseases associated with aberrant BLyS expression
CC   and activity such as cancer, immune, and autoimmune disorders and
CC   diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC   immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC   acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC   the antibodies and fragments of the antibodies described in the method of
CC   the invention
XX
SQ   Sequence 249 AA;

  Query Match             100.0%;  Score 585;  DB 5;  Length 249;
  Best Local Similarity   100.0%;  Pred. No. 1e-36;
  Matches  111;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AFSSELTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 AFSSELTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIP 198

Qy         61 DRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 111
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        199 DRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 249


RESULT 12
ABP44497
ID   ABP44497 standard; protein; 249 AA.
XX
AC   ABP44497;
XX
DT   19-AUG-2002  (first entry)
XX
DE   Human BLyS binding scFv SEQ ID 508.
XX
KW   BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW   tumour necrosis factor; B cell proliferation; B cell differentiation;
KW   immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW   antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW   systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW   common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS   Homo sapiens.
XX
PN   WO200202641-A1.
XX
PD   10-JAN-2002.
XX
PF   15-JUN-2001; 2001WO-US019110.
XX
PR   16-JUN-2000; 2000US-0212210P.
PR   17-OCT-2000; 2000US-0240816P.
PR   16-MAR-2001; 2001US-0276248P.
PR   21-MAR-2001; 2001US-0277379P.
PR   25-MAY-2001; 2001US-0293499P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
PA   (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI   Ruben SM,  Barash SC,  Choi GH,  Vaughan T,  Hilbert D;
XX
DR   WPI; 2002-114799/15.
XX
PT   Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
PT   diagnosis and treatment of cancers and immune disorders.
XX
PS   Claim 1; Page 1009-1010; 3148pp; English.
XX
CC   This invention describes novel antibodies that immunospecifically bind to
CC   B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the
CC   tumour necrosis factor (TNF) super family and induces B cell
CC   proliferation and differentiation. The antibodies of the invention have
CC   cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC   antirheumatic and antiAIDS activity and can be used in vaccines to
CC   inhibit the expression and activity of BLyS. The antibodies bind to BLyS
CC   and so may be used to detect and quantitate the presence of BLyS in
CC   biological samples and may be used in this way to diagnose disease
CC   associated with aberrant expression of BLyS. They may also be
CC   administered to treat diseases associated with aberrant BLyS expression
CC   and activity such as cancer, immune, and autoimmune disorders and
CC   diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC   immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC   acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC   the antibodies and fragments of the antibodies described in the method of
CC   the invention
XX
SQ   Sequence 249 AA;
```

```
  Query Match           100.0%;  Score 585;  DB 5;  Length 249;
  Best Local Similarity  100.0%;  Pred. No. 1e-36;
  Matches  111;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AFSSELTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 AFSSELTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIP 198

Qy         61 DRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 111
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        199 DRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 249


RESULT 13
ABP44548
ID   ABP44548 standard; protein; 249 AA.
XX
AC   ABP44548;
XX
[redacted]   19-AUG-2002  (first entry)

     Human BLyS binding scFv SEQ ID 559.
XX
KW   BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW   tumour necrosis factor; B cell proliferation; B cell differentiation;
KW   immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW   antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW   systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW   common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS   Homo sapiens.
XX
PN   WO200202641-A1.
XX
PD   10-JAN-2002.
XX
PF   15-JUN-2001; 2001WO-US019110.
XX
PR   16-JUN-2000; 2000US-0212210P.
PR   17-OCT-2000; 2000US-0240816P.
PR   16-MAR-2001; 2001US-0276248P.
PR   21-MAR-2001; 2001US-0277379P.
PR   25-MAY-2001; 2001US-0293499P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
PA   (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
[redacted]   Ruben SM,  Barash SC,  Choi GH,  Vaughan T,  Hilbert D;

     WPI; 2002-114799/15.
XX
PT   Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
PT   diagnosis and treatment of cancers and immune disorders.
XX
PS   Claim 1; Page 1069-1070; 3148pp; English.
XX
CC   This invention describes novel antibodies that immunospecifically bind to
CC   B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the
CC   tumour necrosis factor (TNF) super family and induces B cell
CC   proliferation and differentiation. The antibodies of the invention have
CC   cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC   antirheumatic and antiAIDS activity and can be used in vaccines to
CC   inhibit the expression and activity of BLyS. The antibodies bind to BLyS
CC   and so may be used to detect and quantitate the presence of BLyS in
CC   biological samples and may be used in this way to diagnose disease
CC   associated with aberrant expression of BLyS. They may also be
CC   administered to treat diseases associated with aberrant BLyS expression
CC   and activity such as cancer, immune, and autoimmune disorders and
CC   diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC   immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC   acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC   the antibodies and fragments of the antibodies described in the method of
CC   the invention
XX
SQ   Sequence 249 AA;

  Query Match           100.0%;  Score 585;  DB 5;  Length 249;
  Best Local Similarity  100.0%;  Pred. No. 1e-36;
  Matches  111;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AFSSELTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 AFSSELTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIP 198

Qy         61 DRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 111
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        199 DRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 249


RESULT 14
ABP44613
ID   ABP44613 standard; protein; 249 AA.
XX
AC   ABP44613;
XX
DT   19-AUG-2002  (first entry)
XX
DE   Human BLyS binding scFv SEQ ID 624.
XX
KW   BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW   tumour necrosis factor; B cell proliferation; B cell differentiation;
KW   immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW   antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW   systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW   common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS   Homo sapiens.
XX
PN   WO200202641-A1.
XX
PD   10-JAN-2002.
XX
PF   15-JUN-2001; 2001WO-US019110.
XX
PR   16-JUN-2000; 2000US-0212210P.
PR   17-OCT-2000; 2000US-0240816P.
PR   16-MAR-2001; 2001US-0276248P.
PR   21-MAR-2001; 2001US-0277379P.
PR   25-MAY-2001; 2001US-0293499P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
PA   (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI   Ruben SM,  Barash SC,  Choi GH,  Vaughan T,  Hilbert D;
XX
DR   WPI; 2002-114799/15.
XX
PT   Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
PT   diagnosis and treatment of cancers and immune disorders.
XX
PS   Claim 1; Page 1146-1147; 3148pp; English.
XX
CC   This invention describes novel antibodies that immunospecifically bind to
CC   B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the
CC   tumour necrosis factor (TNF) super family and induces B cell
CC   proliferation and differentiation. The antibodies of the invention have
CC   cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC   antirheumatic and antiAIDS activity and can be used in vaccines to
CC   inhibit the expression and activity of BLyS. The antibodies bind to BLyS
CC   and so may be used to detect and quantitate the presence of BLyS in
CC   biological samples and may be used in this way to diagnose disease
CC   associated with aberrant expression of BLyS. They may also be
CC   administered to treat diseases associated with aberrant BLyS expression
CC   and activity such as cancer, immune, and autoimmune disorders and
CC   diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC   immunodeficiency (e.g. common variable immunodeficiency (CVID) and
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CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention
XX
SQ Sequence 249 AA;

Query Match 100.0%; Score 585; DB 5; Length 249;
Best Local Similarity 100.0%; Pred. No. 1e-36;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 139 AFSSELTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIP 198

Qy 61 DRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 111
Db 199 DRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 249

[redacted]LT 15
4621
ID ABP44621 standard; protein; 249 AA.
XX
AC ABP44621;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human BLyS binding scFv SEQ ID 632.
XX
KW BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS Homo sapiens.
XX
PN WO200202641-A1.
XX
PD 10-JAN-2002.
XX
PF 15-JUN-2001; 2001WO-US019110.
XX
PR 16-JUN-2000; 2000US-0212210P.
PR 17-OCT-2000; 2000US-0240816P.
PR 16-MAR-2001; 2001US-0276248P.
PR 21-MAR-2001; 2001US-0277379P.
PR 25-MAY-2001; 2001US-0293499P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX
DR WPI; 2002-114799/15.
XX
PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
PT diagnosis and treatment of cancers and immune disorders.
XX
PS Claim 1; Page 1156-1157; 3148pp; English.
XX
CC This invention describes novel antibodies that immunospecifically bind to
CC B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of BLyS. The antibodies bind to BLyS
CC and so may be used to detect and quantitate the presence of BLyS in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of BLyS. They may also be
CC administered to treat diseases associated with aberrant BLyS expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention
XX
SQ Sequence 249 AA;

Query Match 100.0%; Score 585; DB 5; Length 249;
Best Local Similarity 100.0%; Pred. No. 1e-36;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AFSSELTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIP 60
Db 139 AFSSELTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIP 198

Qy 61 DRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 111
Db 199 DRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 249

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Job time : 48.9103 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: September 9, 2004, 11:04:55 ; Search time 14.2308 Seconds
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402.683 Million cell updates/sec

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Perfect score: 585
Sequence: 1 AFSSELTQDPAVSVALGQTV.....RDSSGNHWVFGGGTELTVLG 111

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

l number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 70 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	556	95.0	278	3	US-09-260-527-3	Sequence 3, Appli
2	556	95.0	280	3	US-09-260-527-1	Sequence 1, Appli
3	556	95.0	309	4	US-09-079-029-9	Sequence 9, Appli
4	556	95.0	312	4	US-09-079-029-10	Sequence 10, Appl
5	540.5	92.4	109	2	US-08-665-202-34	Sequence 34, Appl
6	540.5	92.4	109	4	US-09-315-574-34	Sequence 34, Appl
7	529	90.4	109	2	US-08-652-816A-16	Sequence 16, Appl
8	494	84.4	97	2	US-08-665-202-35	Sequence 35, Appl
9	494	84.4	97	4	US-09-315-574-35	Sequence 35, Appl
10	489.5	83.7	104	4	US-08-793-450-2	Sequence 2, Appli
11	489.5	83.7	238	4	US-08-793-450-6	Sequence 6, Appli
12	475	81.2	104	3	US-09-240-274-49	Sequence 49, Appl
13	468	80.0	106	3	US-09-240-274-48	Sequence 48, Appl
14	468	80.0	106	3	US-09-240-274-50	Sequence 50, Appl
15	463	79.1	103	2	US-08-273-146-71	Sequence 71, Appl
16	461	78.8	106	3	US-09-240-274-47	Sequence 47, Appl
17	436.5	74.6	108	4	US-09-025-769B-20	Sequence 20, Appl
18	431.5	73.8	105	1	US-08-488-113B-157	Sequence 157, App
19	431.5	73.8	105	1	US-08-477-484B-157	Sequence 157, App
20	431.5	73.8	105	1	US-08-107-669D-21	Sequence 21, Appl
21	431.5	73.8	105	1	US-08-472-788A-21	Sequence 21, Appl
22	431.5	73.8	105	2	US-08-477-531B-21	Sequence 21, Appl
23	431.5	73.8	105	2	US-08-646-360-157	Sequence 157, App
24	431.5	73.8	105	2	US-08-082-842A-21	Sequence 21, Appl
25	431.5	73.8	105	3	US-08-839-765-157	Sequence 157, App
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33	417	71.3	108	4	US-08-450-363-12	Sequence 12, Appl
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35	395	67.5	107	4	US-09-025-769B-34	Sequence 34, Appl
36	395	67.5	107	4	US-09-025-769B-55	Sequence 55, Appl
37	391.5	66.9	249	4	US-10-039-785-53	Sequence 53, Appl
38	385	65.8	109	1	US-08-478-039-91	Sequence 91, Appl
39	385	65.8	109	1	US-08-476-349A-91	Sequence 91, Appl
40	381.5	65.2	143	2	US-08-345-321-8	Sequence 8, Appli
41	379	64.8	108	1	US-08-259-372A-10	Sequence 10, Appl
42	379	64.8	108	1	US-08-468-671-10	Sequence 10, Appl
43	379	64.8	234	3	US-08-487-550-2	Sequence 2, Appli
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45	370	63.2	106	1	US-08-259-372A-16	Sequence 16, Appl
46	370	63.2	106	1	US-08-468-671-16	Sequence 16, Appl
47	369	63.1	128	1	US-08-478-039-110	Sequence 110, App
48	369	63.1	128	1	US-08-476-349A-110	Sequence 110, App
49	369	63.1	128	3	US-08-523-894-4	Sequence 4, Appli
50	369	63.1	233	3	US-08-523-894-6	Sequence 6, Appli
51	364	62.2	245	4	US-10-039-785-42	Sequence 42, Appl
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53	362	61.9	109	1	US-08-476-349A-92	Sequence 92, Appl
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56	353.5	60.4	112	4	US-09-315-574-39	Sequence 39, Appl
57	353	60.3	111	2	US-08-665-202-36	Sequence 36, Appl
58	353	60.3	111	4	US-09-315-574-36	Sequence 36, Appl
59	353	60.3	258	2	US-08-665-202-5	Sequence 5, Appli
60	353	60.3	258	4	US-09-315-574-5	Sequence 5, Appli
61	353	60.3	262	4	US-09-069-821-4	Sequence 4, Appli
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63	351.5	60.1	236	3	US-09-049-672A-7	Sequence 7, Appli
64	349.5	59.7	108	3	US-09-240-274-66	Sequence 66, Appl
65	349.5	59.7	110	3	US-09-240-274-63	Sequence 63, Appl
66	348	59.5	111	2	US-08-665-202-40	Sequence 40, Appl
67	348	59.5	111	4	US-09-315-574-40	Sequence 40, Appl
68	347	59.3	111	2	US-08-665-202-43	Sequence 43, Appl
69	347	59.3	111	4	US-09-315-574-43	Sequence 43, Appl
70	347	59.3	245	4	US-10-039-785-48	Sequence 48, Appl

ALIGNMENTS

RESULT 1
US-09-260-527-3
; Sequence 3, Application US/09260527A
; Patent No. 6228599
; GENERAL INFORMATION:
; APPLICANT: Knox, J.P.
; APPLICANT: Mikkelsen, J.D.
; APPLICANT: Willats, W. G.
; TITLE OF INVENTION: ANTIBODY
; FILE REFERENCE: DYOU19.001AUS
; CURRENT APPLICATION NUMBER: US/09/260,527A
; CURRENT FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 278
; TYPE: PRT
; ORGANISM: UNKNOWN
; FEATURE:
; OTHER INFORMATION: Anti-homogalacturonan specific antibodies selected
; OTHER INFORMATION: from a naive phage display library known as the
; OTHER INFORMATION: Synthetic scFv Library (#1) from the Centre for
; OTHER INFORMATION: Protein Engineering, MRC Centre, Cambridge, UK
US-09-260-527-3

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  Best Local Similarity   97.2%;  Pred. No. 1.3e-45;
  Matches  106;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

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RESULT 2
US-09-260-527-1
; Sequence 1, Application US/09260527A
; Patent No. 6228599
; GENERAL INFORMATION:
;  APPLICANT: Knox, J.P.
;  APPLICANT: Mikkelsen, J.D.
;  APPLICANT: Willats, W. G.
;  TITLE OF INVENTION: ANTIBODY
;  FILE REFERENCE: DYOU19.001AUS
;  CURRENT APPLICATION NUMBER: US/09/260,527A
;  CURRENT FILING DATE: 1999-02-26
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
;   LENGTH: 280
;   TYPE: PRT
;   ORGANISM: UNKNOWN
;   FEATURE:
;   OTHER INFORMATION: Anti-homogalacturonan specific antibodies from a
;   OTHER INFORMATION: phage display library known as the Synthetic scFv
;   OTHER INFORMATION: Library (#1) from the Centre for Protein
;   OTHER INFORMATION: Engineering, MRC Centre, Cambridge, UK.
US-09-260-527-1

  Query Match             95.0%;  Score 556;  DB 3;  Length 280;
  Best Local Similarity   97.2%;  Pred. No. 1.3e-45;
  Matches  106;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

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RESULT 3
US-09-079-029-9
; Sequence 9, Application US/09079029
; Patent No. 6342369
;  GENERAL INFORMATION:
;    APPLICANT:  Adams, Camilia W.
;    APPLICANT:  Ashkenazi, Avi J.
;    APPLICANT:  Chuntharapai, Anan
;    APPLICANT:  Kim, Kyung J.
;    TITLE OF INVENTION:  Apo-2 Receptor
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  1 DNA Way
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/079,029
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Marschang, Diane L.
;      REGISTRATION NUMBER:  35,600
;      REFERENCE/DOCKET NUMBER:  P1101R2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650/225-5416
;      TELEFAX:  650/952-9881
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  309 amino acids
;      TYPE:  Amino Acid
;      TOPOLOGY:  Linear
US-09-079-029-9

  Query Match             95.0%;  Score 556;  DB 4;  Length 309;
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US-09-079-029-10
; Sequence 10, Application US/09079029
; Patent No. 6342369
;  GENERAL INFORMATION:
;    APPLICANT:  Adams, Camilia W.
;    APPLICANT:  Ashkenazi, Avi J.
;    APPLICANT:  Chuntharapai, Anan
;    APPLICANT:  Kim, Kyung J.
;    TITLE OF INVENTION:  Apo-2 Receptor
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  1 DNA Way
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/079,029
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Marschang, Diane L.
;      REGISTRATION NUMBER:  35,600
;      REFERENCE/DOCKET NUMBER:  P1101R2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650/225-5416
;      TELEFAX:  650/952-9881
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  312 amino acids
;      TYPE:  Amino Acid
;      TOPOLOGY:  Linear
US-09-079-029-10
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  Query Match             95.0%;  Score 556;  DB 4;  Length 312;
  Best Local Similarity   97.2%;  Pred. No. 1.5e-45;
  Matches  106;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 SSELTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIPDR 62
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RESULT 5
US-08-665-202-34
; Sequence 34, Application US/08665202
; Patent No. 5977322
;  GENERAL INFORMATION:
;    APPLICANT:  Marks, James D.
;    APPLICANT:  Schier, Robert
;    TITLE OF INVENTION:  No. 5977322el High Affinity Human Antibodies to
;    TITLE OF INVENTION:  Tumor Antigens
;    NUMBER OF SEQUENCES:  141
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/665,202
;      FILING DATE:  13-JUN-1996
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/000,238
;      FILING DATE:  14-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/000,250
;      FILING DATE:  15-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hunter, Tom
;      REGISTRATION NUMBER:  38,498
;      REFERENCE/DOCKET NUMBER:  02307E-061410
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  34:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  109 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-665-202-34

  Query Match             92.4%;  Score 540.5;  DB 2;  Length 109;
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Db         61 SGSSSGNIASLTITGAQAEDEADYYCNSRDSSGNPYWVFGGGTKVTVLG 109


RESULT 6
US-09-315-574-34
; Sequence 34, Application US/09315574
; Patent No. 6512097
;  GENERAL INFORMATION:
;    APPLICANT:  Marks, James D.
;    APPLICANT:  Schier, Robert
;    TITLE OF INVENTION:  No. 6512097el High Affinity Human Antibodies to
;    TITLE OF INVENTION:  Tumor Antigens
;    NUMBER OF SEQUENCES:  141
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Majestic, Parsons, Siebert & Hsue P.C.
;      STREET:  Four Embarcadero Center, Suite 1100
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-4106
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/315,574
;      FILING DATE:  20-MAY-99
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/000,238
;      FILING DATE:  14-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/000,250
;      FILING DATE:  15-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/665,202
;      FILING DATE:  13-JUN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hunter, Tom
;      REGISTRATION NUMBER:  38,498
;      REFERENCE/DOCKET NUMBER:  02307E-061411
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  34:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  109 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-315-574-34

  Query Match             92.4%;  Score 540.5;  DB 4;  Length 109;
  Best Local Similarity   94.5%;  Pred. No. 1.3e-44;
  Matches  103;  Conservative    4;  Mismatches    1;  Indels    1;  Gaps    1;

Qy          4 SELTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIPDRF 63
              |||||||||||||||||:||||||||||||||||||||||||||||||||||||||||||
Db          1 SELTQDPAVSVALGQTVRITCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIPDRF 60

Qy         64 SGSSSGNTASLTITGAQAEDEADYYCNSRDSSGN-HWVFGGGTELTVLG 111
              ||||||| |||||||||||||||||||||||| :|||||||::||||
Db         61 SGSSSGNIASLTITGAQAEDEADYYCNSRDSSGNPYWVFGGGTKVTVLG 109


RESULT 7
US-08-652-816A-16
; Sequence 16, Application US/08652816A
; Patent No. 5872215
;  GENERAL INFORMATION:
;    APPLICANT:  Osbourn, JK
;    APPLICANT:  Allen, DJ
;    APPLICANT:  McCafferty, JG
```

```
;    TITLE OF INVENTION:  Specific binding members, materials and
;    TITLE OF INVENTION:  methods.
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States of America
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/652,816A
;      FILING DATE:  23-MAY-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9125579.4
;      FILING DATE:  02-DEC-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9125579.8
;      FILING DATE:  02-DEC-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9206318.9
;      FILING DATE:  24-MAR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9206372.6
;      FILING DATE:  23-SEP-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9525004.9
;      FILING DATE:  07-DEC-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9610824.6
;      FILING DATE:  23-MAY-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/GB92/02240
;      FILING DATE:  02-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/244,597
;      FILING DATE:  01-JUN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  David W. Clough
;      REGISTRATION NUMBER:  36,107
;      REFERENCE/DOCKET NUMBER:  28111/33308
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-474-6300
;  INFORMATION FOR SEQ ID NO:  16:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  109 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-08-652-816A-16

  Query Match             90.4%;  Score 529;  DB 2;  Length 109;
  Best Local Similarity   93.5%;  Pred. No. 1.7e-43;
  Matches  100;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          3 SSELTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIPDR 62
              |||||||||||| |||||:|||||||||||||||||||| ||||||||||||||||||
Db          1 SSELTQDPAVSVPLGQTVRITCQGDSLRSYYASWYQQKPGQPPVLVIYGKNNRPSGIPDR 60

Qy         63 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTV 109
              ||||||||||||||||||||||||||||||||||| |||||:| :
Db         61 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVVFGGGTKLEI 107


RESULT 8
US-08-665-202-35
; Sequence 35, Application US/08665202
; Patent No. 5977322
;  GENERAL INFORMATION:
;    APPLICANT:  Marks, James D.
;    APPLICANT:  Schier, Robert
;    TITLE OF INVENTION:  No. 5977322el High Affinity Human Antibodies to
;    TITLE OF INVENTION:  Tumor Antigens
;    NUMBER OF SEQUENCES:  141
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/665,202
;      FILING DATE:  13-JUN-1996
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/000,238
;      FILING DATE:  14-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/000,250
;      FILING DATE:  15-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hunter, Tom
;      REGISTRATION NUMBER:  38,498
;      REFERENCE/DOCKET NUMBER:  02307E-061410
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  35:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  97 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-665-202-35

  Query Match             84.4%;  Score 494;  DB 2;  Length 97;
  Best Local Similarity   96.9%;  Pred. No. 3.2e-40;
  Matches   94;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 SELTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIPDRF 63
              | ||||||||||||||||:|||||||||||||||||||||||||||||||||||||||
Db          1 SSLTQDPAVSVALGQTVRITCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIPDRF 60

Qy         64 SGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWV 100
              |||||||||||||||||||||||||||||||||| |
Db         61 SGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVV 97


RESULT 9
US-09-315-574-35
; Sequence 35, Application US/09315574
; Patent No. 6512097
;  GENERAL INFORMATION:
;    APPLICANT:  Marks, James D.
;    APPLICANT:  Schier, Robert
;    TITLE OF INVENTION:  No. 6512097el High Affinity Human Antibodies to
;    TITLE OF INVENTION:  Tumor Antigens
;    NUMBER OF SEQUENCES:  141
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Majestic, Parsons, Siebert & Hsue P.C.
;      STREET:  Four Embarcadero Center, Suite 1100
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-4106
;    COMPUTER READABLE FORM:
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```
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/315,574
;       FILING DATE:  20-MAY-99
;       CLASSIFICATION:  530
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 60/000,238
;       FILING DATE:  14-JUN-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 60/000,250
;       FILING DATE:  15-JUN-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/665,202
;       FILING DATE:  13-JUN-1996
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Hunter, Tom
;       REGISTRATION NUMBER:  38,498
;       REFERENCE/DOCKET NUMBER:  02307E-061411
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (415) 576-0200
;       TELEFAX:  (415) 576-0300
;   INFORMATION FOR SEQ ID NO:  35:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  97 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
US-09-315-574-35

  Query Match             84.4%;  Score 494;  DB 4;  Length 97;
  Best Local Similarity   96.9%;  Pred. No. 3.2e-40;
  Matches   94;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 SELTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIPDRF 63
              | ||||||||||||||||:|||||||||||||||||||||||||||||||||||||||||
Db          1 SSLTQDPAVSVALGQTVRITCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIPDRF 60

Qy         64 SGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWV 100
              |||||||||||||||||||||||||||||||| |
Db         61 SGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVV 97


RESULT 10
US-08-793-450-2
; Sequence 2, Application US/08793450
; Patent No. 6312690
;  GENERAL INFORMATION:
;    APPLICANT:  EDELMAN, LENA
;    APPLICANT:  MARGARITTE, CHRISTEL
;    APPLICANT:  KACZOREK, MICHEL
;    APPLICANT:  CHAABIHI, HASSAN
;    TITLE OF INVENTION:  MONOCLONAL RECOMBINANT ANTI-RHESUS D
;    TITLE OF INVENTION:
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
;      ADDRESSEE:  P.C.
;      STREET:  1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/793,450
;      FILING DATE:  03-MAR-1997
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  FR 94/10566
;      FILING DATE:  02-SEP-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  OBLON, NORMAN F.
;      REGISTRATION NUMBER:  24,618
;      REFERENCE/DOCKET NUMBER:  660-118-0 PCT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-413-3000
;      TELEFAX:  703-413-2220
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  104 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-793-450-2

  Query Match             83.7%;  Score 489.5;  DB 4;  Length 104;
  Best Local Similarity   88.8%;  Pred. No. 9.3e-40;
  Matches   95;  Conservative    4;  Mismatches    3;  Indels    5;  Gaps    1;

Qy          5 ELTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIPDRFS 64
              |||||||||||||||||:||||||||:||||||||||||||||||||||||||||||||
Db          3 ELTQDPAVSVALGQTVRITCQGDSLRTYYASWYQQKPGQAPVLVIYGKNNRPSGIPDRFS 62

Qy         65 GSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 111
              |||||||||||||||||||||||:||  .      ||||||:|||||
Db         63 GSSSGNTASLTITGAQAEDEADYFCNSGGK-----VFGGGTKLTVLG 104


RESULT 11
US-08-793-450-6
; Sequence 6, Application US/08793450
; Patent No. 6312690
;  GENERAL INFORMATION:
;    APPLICANT:  EDELMAN, LENA
;    APPLICANT:  MARGARITTE, CHRISTEL
;    APPLICANT:  KACZOREK, MICHEL
;    APPLICANT:  CHAABIHI, HASSAN
;    TITLE OF INVENTION:  MONOCLONAL RECOMBINANT ANTI-RHESUS D
;    TITLE OF INVENTION:
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
;      ADDRESSEE:  P.C.
;      STREET:  1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/793,450
;      FILING DATE:  03-MAR-1997
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  FR 94/10566
;      FILING DATE:  02-SEP-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  OBLON, NORMAN F.
;      REGISTRATION NUMBER:  24,618
;      REFERENCE/DOCKET NUMBER:  660-118-0 PCT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-413-3000
;      TELEFAX:  703-413-2220
;  INFORMATION FOR SEQ ID NO:  6:
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;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  238 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-793-450-6

  Query Match             83.7%;  Score 489.5;  DB 4;  Length 238;
  Best Local Similarity   88.8%;  Pred. No. 2.4e-39;
  Matches   95;  Conservative    4;  Mismatches    3;  Indels    5;  Gaps    1;

Qy          5 ELTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIPDRFS 64
              |||||||||||||||||:||||||||:||||||||||||||||||||||||||||||||
Db         22 ELTQDPAVSVALGQTVRITCQGDSLRTYYASWYQQKPGQAPVLVIYGKNNRPSGIPDRFS 81

Qy         65 GSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 111
              |||||||||||||||||||||:|||       ||||||:|||||
Db         82 GSSSGNTASLTITGAQAEDEADYFCNSGGK-----VFGGGTKLTVLG 123


RESULT 12
US-09-240-274-49
; Sequence 49, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/240,274
;  CURRENT FILING DATE: 1999-01-29
;  EARLIER APPLICATION NUMBER: 60/081,380
;  EARLIER FILING DATE: 1998-04-10
;  EARLIER APPLICATION NUMBER: 60/028,550
;  EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 49
;   LENGTH: 104
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) chain J04
US-09-240-274-49

  Query Match             81.2%;  Score 475;  DB 3;  Length 104;
  Best Local Similarity   89.3%;  Pred. No. 2.3e-38;
  Matches   92;  Conservative    4;  Mismatches    5;  Indels    2;  Gaps    1;

Qy          8 QDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIPDRFSGSS 67
              ||| ||||||||||:||||||||||||||||||||||||:|||||||||||||
Db          4 QDPVVSVALGQTVRITCQGDSLRSYYASWYQQKPGQAPVLVIYGKNSRPSGIPDRFSGSS 63

Qy         68 SGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVL 110
              |||||||||||||||||||:|| |   |  |||||:||||
Db         64 SGNTASLTITGAQAEDEADYYCSSRGSP--HVAFGGGTKLTVL 104


RESULT 13
US-09-240-274-48
; Sequence 48, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/240,274
;  CURRENT FILING DATE: 1999-01-29
;  EARLIER APPLICATION NUMBER: 60/081,380
;  EARLIER FILING DATE: 1998-04-10
;  EARLIER APPLICATION NUMBER: 60/028,550
;  EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
;   LENGTH: 106
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) chain J02
US-09-240-274-48

  Query Match             80.0%;  Score 468;  DB 3;  Length 106;
  Best Local Similarity   85.4%;  Pred. No. 1.1e-37;
  Matches   88;  Conservative    6;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          8 QDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIPDRFSGSS 67
              ||| ||||||||||:||||| |||||||||||||||| ||:||:|||||||||||||||
Db          4 QDPVVSVALGQTVRITCQGDGLRSYYASWYQQKPGQAPKLVMYGRNNRPSGIPDRFSGSS 63

Qy         68 SGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVL 110
              || ||:||||| |||||||||| || :|||  ||||||:||||
Db         64 SGQTAALTITGTQAEDEADYYCQSRATSGNPVVFGGGTKLTVL 106


RESULT 14
US-09-240-274-50
; Sequence 50, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/240,274
;  CURRENT FILING DATE: 1999-01-29
;  EARLIER APPLICATION NUMBER: 60/081,380
;  EARLIER FILING DATE: 1998-04-10
;  EARLIER APPLICATION NUMBER: 60/028,550
;  EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 50
;   LENGTH: 106
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) chain J05
US-09-240-274-50

  Query Match             80.0%;  Score 468;  DB 3;  Length 106;
  Best Local Similarity   83.5%;  Pred. No. 1.1e-37;
  Matches   86;  Conservative   10;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          8 QDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIPDRFSGSS 67
              ||| |||||||||::|||||||| |||||||||||||||| | :|:|||||||||||||:
Db          4 QDPVVSVALGQTVKITCQGDSLRKYYASWYQQKPGQAPVLVFYARNSRPSGIPDRFSGSN 63

Qy         68 SGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVL 110
              || |||||| ||:||||||||:||||:|:| ||||||:||||
Db         64 SGTTASLTIAGARAEDEADYYCHSRDSNGHHRVFGGGTKLTVL 106


RESULT 15
US-08-273-146-71
; Sequence 71, Application US/08273146
; Patent No. 5855885
;  GENERAL INFORMATION:
;    APPLICANT:  Smith, Rodger
;    APPLICANT:  McCafferty, John
;    APPLICANT:  Chiswell, David
;    APPLICANT:  Darsley, Michael J.
;    APPLICANT:  Fitzgerald, Kevin
;    APPLICANT:  Kenten, John H.
;    APPLICANT:  Martin, Mark T.
```

; APPLICANT: Titmas, Richard C.
; APPLICANT: Williams, Richard O.
; TITLE OF INVENTION: The Isolation and Production of
; TITLE OF INVENTION: Catalytic Antibodies using Phage Technology
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IGEN, Inc.
; STREET: 1530 East Jefferson St.
; CITY: Rockville
; STATE: MD
; COUNTRY: USA
; ZIP: 20852
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/273,146
; FILING DATE: 14-JUL-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ryan, John W.
; REGISTRATION NUMBER: 33,771
; REFERENCE/DOCKET NUMBER: 09000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-984-8000
; TELEFAX: 301-230-0158
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 103 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-273-146-71

Query Match 79.1%; Score 463; DB 2; Length 103;
Best Local Similarity 90.8%; Pred. No. 3.1e-37;
Matches 89; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

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Qy          74 LTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 111
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Db          66 LTITGAQAEDEADYYCLSRDSGSNQLVFGGGTKLTVLG 103
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Search completed: September 9, 2004, 11:09:20
Job time : 16.2308 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: September 9, 2004, 11:07:30 ; Search time 81.5897 Seconds
(without alignments)
436.287 Million cell updates/sec

Title: US-09-880-748-2_COPY_139_249
Perfect score: 585
Sequence: 1 AFSSELTQDPAVSVALGQTV.....RDSSGNHWVFGGGTELTVLG 111

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1335176 seqs, 320689617 residues

l number of hits satisfying chosen parameters: 1335176

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 70 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
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18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	585	100.0	248	10	US-09-880-748-339	Sequence 339, App
2	585	100.0	248	10	US-09-880-748-347	Sequence 347, App
3	585	100.0	248	10	US-09-880-748-354	Sequence 354, App
4	585	100.0	248	10	US-09-880-748-597	Sequence 597, App
5	585	100.0	248	10	US-09-880-748-623	Sequence 623, App
6	585	100.0	248	12	US-10-293-418-339	Sequence 339, App
7	585	100.0	248	12	US-10-293-418-347	Sequence 347, App
8	585	100.0	248	12	US-10-293-418-354	Sequence 354, App
9	585	100.0	248	12	US-10-293-418-597	Sequence 597, App
10	585	100.0	248	12	US-10-293-418-623	Sequence 623, App
11	585	100.0	249	10	US-09-880-748-2	Sequence 2, Appli
12	585	100.0	249	10	US-09-880-748-323	Sequence 323, App
13	585	100.0	249	10	US-09-880-748-324	Sequence 324, App
14	585	100.0	249	10	US-09-880-748-326	Sequence 326, App
15	585	100.0	249	10	US-09-880-748-332	Sequence 332, App
16	585	100.0	249	10	US-09-880-748-333	Sequence 333, App
17	585	100.0	249	10	US-09-880-748-334	Sequence 334, App
18	585	100.0	249	10	US-09-880-748-335	Sequence 335, App
19	585	100.0	249	10	US-09-880-748-336	Sequence 336, App
20	585	100.0	249	10	US-09-880-748-338	Sequence 338, App
21	585	100.0	249	10	US-09-880-748-342	Sequence 342, App
22	585	100.0	249	10	US-09-880-748-343	Sequence 343, App
23	585	100.0	249	10	US-09-880-748-344	Sequence 344, App
24	585	100.0	249	10	US-09-880-748-345	Sequence 345, App
25	585	100.0	249	10	US-09-880-748-348	Sequence 348, App
26	585	100.0	249	10	US-09-880-748-349	Sequence 349, App
27	585	100.0	249	10	US-09-880-748-350	Sequence 350, App
28	585	100.0	249	10	US-09-880-748-352	Sequence 352, App
29	585	100.0	249	10	US-09-880-748-355	Sequence 355, App
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32	585	100.0	249	10	US-09-880-748-358	Sequence 358, App
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34	585	100.0	249	10	US-09-880-748-360	Sequence 360, App
35	585	100.0	249	10	US-09-880-748-361	Sequence 361, App
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43	585	100.0	249	10	US-09-880-748-371	Sequence 371, App
44	585	100.0	249	10	US-09-880-748-372	Sequence 372, App
45	585	100.0	249	10	US-09-880-748-373	Sequence 373, App
46	585	100.0	249	10	US-09-880-748-375	Sequence 375, App
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48	585	100.0	249	10	US-09-880-748-377	Sequence 377, App
49	585	100.0	249	10	US-09-880-748-379	Sequence 379, App
50	585	100.0	249	10	US-09-880-748-381	Sequence 381, App
51	585	100.0	249	10	US-09-880-748-382	Sequence 382, App
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55	585	100.0	249	10	US-09-880-748-387	Sequence 387, App
56	585	100.0	249	10	US-09-880-748-388	Sequence 388, App
57	585	100.0	249	10	US-09-880-748-390	Sequence 390, App
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61	585	100.0	249	10	US-09-880-748-396	Sequence 396, App
62	585	100.0	249	10	US-09-880-748-398	Sequence 398, App
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64	585	100.0	249	10	US-09-880-748-400	Sequence 400, App
65	585	100.0	249	10	US-09-880-748-402	Sequence 402, App
66	585	100.0	249	10	US-09-880-748-403	Sequence 403, App
67	585	100.0	249	10	US-09-880-748-404	Sequence 404, App
68	585	100.0	249	10	US-09-880-748-405	Sequence 405, App
69	585	100.0	249	10	US-09-880-748-406	Sequence 406, App
70	585	100.0	249	10	US-09-880-748-408	Sequence 408, App

ALIGNMENTS

RESULT 1
US-09-880-748-339
; Sequence 339, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816

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;  PRIOR FILING DATE: 2000-10-17
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  NUMBER OF SEQ ID NOS: 3239
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 339
;   LENGTH: 248
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-880-748-339

  Query Match           100.0%;  Score 585;  DB 10;  Length 248;
  Best Local Similarity  100.0%;  Pred. No. 1.7e-45;
  Matches  111;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy         61 DRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 111
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Db        198 DRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 248


RESULT 2
US-09-880-748-347
; Sequence 347, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523
;  CURRENT APPLICATION NUMBER: US/09/880,748
;  CURRENT FILING DATE:  2001-06-15
;  PRIOR APPLICATION NUMBER: 60/212,210
;  PRIOR FILING DATE: 2000-06-15
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  NUMBER OF SEQ ID NOS: 3239
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 347
;   LENGTH: 248
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-880-748-347

  Query Match           100.0%;  Score 585;  DB 10;  Length 248;
  Best Local Similarity  100.0%;  Pred. No. 1.7e-45;
  Matches  111;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AFSSELTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy         61 DRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 111
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Db        198 DRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 248


RESULT 3
US-09-880-748-354
; Sequence 354, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523
;  CURRENT APPLICATION NUMBER: US/09/880,748
;  CURRENT FILING DATE:  2001-06-15
;  PRIOR APPLICATION NUMBER: 60/212,210
;  PRIOR FILING DATE: 2000-06-15
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  NUMBER OF SEQ ID NOS: 3239
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 354
;   LENGTH: 248
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-880-748-354

  Query Match           100.0%;  Score 585;  DB 10;  Length 248;
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  Matches  111;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AFSSELTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy         61 DRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 111
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Db        198 DRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 248


RESULT 4
US-09-880-748-597
; Sequence 597, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523
;  CURRENT APPLICATION NUMBER: US/09/880,748
;  CURRENT FILING DATE:  2001-06-15
;  PRIOR APPLICATION NUMBER: 60/212,210
;  PRIOR FILING DATE: 2000-06-15
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  NUMBER OF SEQ ID NOS: 3239
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 597
;   LENGTH: 248
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-880-748-597

  Query Match           100.0%;  Score 585;  DB 10;  Length 248;
  Best Local Similarity  100.0%;  Pred. No. 1.7e-45;
  Matches  111;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AFSSELTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIP 60
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Qy          61 DRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 111
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Db         198 DRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 248


RESULT 5
US-09-880-748-623
; Sequence 623, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523
;  CURRENT APPLICATION NUMBER: US/09/880,748
;  CURRENT FILING DATE:  2001-06-15
;  PRIOR APPLICATION NUMBER: 60/212,210
;  PRIOR FILING DATE: 2000-06-15
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  NUMBER OF SEQ ID NOS: 3239
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 623
;   LENGTH: 248
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-880-748-623

  Query Match           100.0%;  Score 585;  DB 10;  Length 248;
  Best Local Similarity  100.0%;  Pred. No. 1.7e-45;
  Matches  111;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           1 AFSSELTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIP 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         138 AFSSELTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIP 197

Qy          61 DRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 111
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Db         198 DRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 248


RESULT 6
US-10-293-418-339
; Sequence 339, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523P2
;  CURRENT APPLICATION NUMBER: US/10/293,418
;  CURRENT FILING DATE:  2002-11-27
;  PRIOR APPLICATION NUMBER: 60/331,469
;  PRIOR FILING DATE: 2001-11-16
;  PRIOR APPLICATION NUMBER: 60/340,817
;  PRIOR FILING DATE: 2001-12-19
;  PRIOR APPLICATION NUMBER: 09/880,748
;  PRIOR FILING DATE: 2001-06-15
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  PRIOR APPLICATION NUMBER: 60/212,210
;  PRIOR FILING DATE: 2000-06-16
;  NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 339
;   LENGTH: 248
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-293-418-339

  Query Match           100.0%;  Score 585;  DB 12;  Length 248;
  Best Local Similarity  100.0%;  Pred. No. 1.7e-45;
  Matches  111;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           1 AFSSELTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIP 60
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Db         138 AFSSELTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIP 197

Qy          61 DRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 111
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Db         198 DRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 248


RESULT 7
US-10-293-418-347
; Sequence 347, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523P2
;  CURRENT APPLICATION NUMBER: US/10/293,418
;  CURRENT FILING DATE:  2002-11-27
;  PRIOR APPLICATION NUMBER: 60/331,469
;  PRIOR FILING DATE: 2001-11-16
;  PRIOR APPLICATION NUMBER: 60/340,817
;  PRIOR FILING DATE: 2001-12-19
;  PRIOR APPLICATION NUMBER: 09/880,748
;  PRIOR FILING DATE: 2001-06-15
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  PRIOR APPLICATION NUMBER: 60/212,210
;  PRIOR FILING DATE: 2000-06-16
;  NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 347
;   LENGTH: 248
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-293-418-347

  Query Match           100.0%;  Score 585;  DB 12;  Length 248;
  Best Local Similarity  100.0%;  Pred. No. 1.7e-45;
  Matches  111;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           1 AFSSELTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIP 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         138 AFSSELTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIP 197

Qy          61 DRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 111
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Db         198 DRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 248


RESULT 8
US-10-293-418-354
; Sequence 354, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523P2
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;  CURRENT APPLICATION NUMBER: US/10/293,418
;  CURRENT FILING DATE:  2002-11-27
;  PRIOR APPLICATION NUMBER: 60/331,469
;  PRIOR FILING DATE: 2001-11-16
;  PRIOR APPLICATION NUMBER: 60/340,817
;  PRIOR FILING DATE: 2001-12-19
;  PRIOR APPLICATION NUMBER: 09/880,748
;  PRIOR FILING DATE: 2001-06-15
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  PRIOR APPLICATION NUMBER: 60/212,210
;  PRIOR FILING DATE: 2000-06-16
;  NUMBER OF SEQ ID NOS: 3247
;  SEQ ID NO 354
;    LENGTH: 248
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-10-293-418-354

  Query Match           100.0%;  Score 585;  DB 12;  Length 248;
  Best Local Similarity  100.0%;  Pred. No. 1.7e-45;
  Matches  111;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AFSSELTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        138 AFSSELTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIP 197

Qy         61 DRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 111
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        198 DRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 248


RESULT 9
US-10-293-418-597
; Sequence 597, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523P2
;  CURRENT APPLICATION NUMBER: US/10/293,418
;  CURRENT FILING DATE:  2002-11-27
;  PRIOR APPLICATION NUMBER: 60/331,469
;  PRIOR FILING DATE: 2001-11-16
;  PRIOR APPLICATION NUMBER: 60/340,817
;  PRIOR FILING DATE: 2001-12-19
;  PRIOR APPLICATION NUMBER: 09/880,748
;  PRIOR FILING DATE: 2001-06-15
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  PRIOR APPLICATION NUMBER: 60/212,210
;  PRIOR FILING DATE: 2000-06-16
;  NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 597
;   LENGTH: 248
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-293-418-597

  Query Match           100.0%;  Score 585;  DB 12;  Length 248;
  Best Local Similarity  100.0%;  Pred. No. 1.7e-45;
  Matches  111;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AFSSELTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        138 AFSSELTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIP 197

Qy         61 DRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 111
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        198 DRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 248


RESULT 10
US-10-293-418-623
; Sequence 623, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523P2
;  CURRENT APPLICATION NUMBER: US/10/293,418
;  CURRENT FILING DATE:  2002-11-27
;  PRIOR APPLICATION NUMBER: 60/331,469
;  PRIOR FILING DATE: 2001-11-16
;  PRIOR APPLICATION NUMBER: 60/340,817
;  PRIOR FILING DATE: 2001-12-19
;  PRIOR APPLICATION NUMBER: 09/880,748
;  PRIOR FILING DATE: 2001-06-15
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  PRIOR APPLICATION NUMBER: 60/212,210
;  PRIOR FILING DATE: 2000-06-16
;  NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 623
;   LENGTH: 248
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-293-418-623

  Query Match           100.0%;  Score 585;  DB 12;  Length 248;
  Best Local Similarity  100.0%;  Pred. No. 1.7e-45;
  Matches  111;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AFSSELTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        138 AFSSELTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIP 197

Qy         61 DRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 111
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        198 DRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 248


RESULT 11
US-09-880-748-2
; Sequence 2, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523
;  CURRENT APPLICATION NUMBER: US/09/880,748
;  CURRENT FILING DATE:  2001-06-15
;  PRIOR APPLICATION NUMBER: 60/212,210
;  PRIOR FILING DATE: 2000-06-15
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
```

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;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  NUMBER OF SEQ ID NOS: 3239
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 249
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-880-748-2

  Query Match            100.0%;  Score 585;  DB 10;  Length 249;
  Best Local Similarity  100.0%;  Pred. No. 1.7e-45;
  Matches  111;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AFSSELTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 AFSSELTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIP 198

Qy         61 DRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 111
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        199 DRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 249


RESULT 12
US-09-880-748-323
; Sequence 323, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523
;  CURRENT APPLICATION NUMBER: US/09/880,748
;  CURRENT FILING DATE:  2001-06-15
;  PRIOR APPLICATION NUMBER: 60/212,210
;  PRIOR FILING DATE: 2000-06-15
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  NUMBER OF SEQ ID NOS: 3239
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 323
;   LENGTH: 249
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-880-748-323

  Query Match            100.0%;  Score 585;  DB 10;  Length 249;
  Best Local Similarity  100.0%;  Pred. No. 1.7e-45;
  Matches  111;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AFSSELTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 AFSSELTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIP 198

Qy         61 DRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 111
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        199 DRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 249


RESULT 13
US-09-880-748-324
; Sequence 324, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523
;  CURRENT APPLICATION NUMBER: US/09/880,748
;  CURRENT FILING DATE:  2001-06-15
;  PRIOR APPLICATION NUMBER: 60/212,210
;  PRIOR FILING DATE: 2000-06-15
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  NUMBER OF SEQ ID NOS: 3239
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 324
;   LENGTH: 249
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-880-748-324

  Query Match            100.0%;  Score 585;  DB 10;  Length 249;
  Best Local Similarity  100.0%;  Pred. No. 1.7e-45;
  Matches  111;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AFSSELTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 AFSSELTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIP 198

Qy         61 DRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 111
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        199 DRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 249


RESULT 14
US-09-880-748-326
; Sequence 326, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523
;  CURRENT APPLICATION NUMBER: US/09/880,748
;  CURRENT FILING DATE:  2001-06-15
;  PRIOR APPLICATION NUMBER: 60/212,210
;  PRIOR FILING DATE: 2000-06-15
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  NUMBER OF SEQ ID NOS: 3239
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 326
;   LENGTH: 249
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-880-748-326

  Query Match            100.0%;  Score 585;  DB 10;  Length 249;
  Best Local Similarity  100.0%;  Pred. No. 1.7e-45;
  Matches  111;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AFSSELTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 AFSSELTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIP 198

Qy         61 DRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 111
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        199 DRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 249
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RESULT 15
US-09-880-748-332
; Sequence 332, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 332
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-332

Query Match 100.0%; Score 585; DB 10; Length 249;
Best Local Similarity 100.0%; Pred. No. 1.7e-45;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 AFSSELTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 AFSSELTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIP 198

Qy         61 DRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 111
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        199 DRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 249
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Search completed: September 9, 2004, 11:23:43
Job time : 82.5897 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: September 9, 2004, 10:59:50 ; Search time 12.3333 Seconds
(without alignments)
865.724 Million cell updates/sec

Title: US-09-880-748-2_COPY_139_249
Perfect score: 585
Sequence: 1 AFSSELTQDPAVSVALGQTV.....RDSSGNHWVFGGGTELTVLG 111

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 70 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	556	95.0	109	2	S19663	Ig lambda chain V
2	550	94.0	108	2	S38498	Ig lambda chain -
3	550	94.0	108	2	S47184	Ig lambda chain -
4	544	93.0	127	2	S70444	Ig lambda chain pr
5	539.5	92.2	110	2	S36272	Ig lambda chain V
6	527	90.1	109	2	S38496	Ig lambda chain -
7	518	88.5	233	2	S25748	Ig lambda chain -
8	515	88.0	108	1	L3HUSH	Ig lambda chain V-
9	510.5	87.3	110	2	S19672	Ig lambda chain V
10	505.5	86.4	146	2	S02083	Ig lambda chain V-
11	502	85.8	96	2	S36060	Ig lambda chain -
12	502	85.8	115	2	S13726	Ig lambda chain V
13	494	84.4	233	2	S25741	Ig lambda chain -
14	430.5	73.6	106	2	S38495	Ig lambda chain -
15	408	69.7	105	2	S49533	anti-Sm antibody V
16	407	69.6	119	2	S30526	Ig lambda chain V
17	407	69.6	190	2	S25740	Ig lambda chain -
18	385.5	65.9	120	2	S30525	Ig lambda chain V
19	385	65.8	107	2	PC4283	anti-SS-A/Ro 60K p
20	381	65.1	226	2	S25745	Ig lambda chain -
21	376	64.3	231	2	S25738	Ig lambda chain -
22	375.5	64.2	212	2	S70431	Ig lambda chain -
23	374	63.9	120	2	S30527	Ig lambda chain V
24	372	63.6	151	2	S25739	Ig lambda chain -
25	371	63.4	231	2	S25751	Ig lambda chain -
26	367	62.7	107	1	L4HUHL	Ig lambda chain V-
27	366	62.6	231	2	S25753	Ig lambda chain -
28	364	62.2	109	2	S68171	Ig lambda chain V
29	362	61.9	111	2	S36274	Ig lambda chain V
30	362	61.9	233	2	S25747	Ig lambda chain -
31	358	61.2	108	1	L5HUDL	Ig lambda chain V-
32	357	61.0	106	1	L4HUBU	Ig lambda chain V-
33	355	60.7	132	2	S09713	Ig lambda chain V
34	351.5	60.1	112	2	S51148	antibody light cha
35	351.5	60.1	232	2	S25756	Ig lambda chain -
36	350	59.8	106	1	L4HUML	Ig lambda chain V-
37	348	59.5	106	1	L4HUX	Ig lambda chain V-
38	346.5	59.2	236	2	S25746	Ig lambda chain -
39	346	59.1	105	2	S44124	Ig lambda chain V
40	344	58.8	130	1	L1HUBL	Ig lambda chain pr
41	343	58.6	110	2	S57442	Ig lambda chain V-
42	342	58.5	95	2	S36065	Ig lambda chain -
43	342	58.5	114	2	S16440	Ig lambda chain -
44	341	58.3	128	2	S24319	Ig lambda chain pr
45	340	58.1	235	2	S05270	Ig lambda chain pr
46	339.5	58.0	112	2	S31515	Ig lambda chain V
47	339	57.9	111	1	L2HUMC	Ig lambda chain V-
48	339	57.9	111	2	S47009	Ig lambda chain V1
49	337.5	57.7	110	2	S51149	antibody light cha
50	336	57.4	129	2	S78058	Ig lambda chain pr
51	334	57.1	235	2	S14675	Ig lambda chain -
52	333.5	57.0	112	2	S44105	Ig lambda chain V-
53	333	56.9	106	1	L4HUKN	Ig lambda chain V-
54	333	56.9	125	2	A31493	Ig light chain pre
55	333	56.9	216	2	A42193	Ig lambda chain (B
56	332.5	56.8	112	2	S44123	Ig lambda chain V-
57	330	56.4	111	1	L2HUBH	Ig lambda chain V-
58	330	56.4	111	2	S47185	Ig lambda chain -
59	327	55.9	111	1	L1HUNG	Ig lambda chain V-
60	326.5	55.8	217	2	JE0246	Ig lambda chain NI
61	326	55.7	130	2	S09712	Ig lambda chain V
62	325	55.6	111	1	L2HUVL	Ig lambda chain V-
63	325	55.6	120	2	S30528	Ig lambda chain V
64	325	55.6	232	2	S25742	Ig lambda chain -
65	325	55.6	233	2	S25752	Ig lambda chain -
66	324	55.4	136	2	S16848	Ig lambda chain V-
67	324	55.4	213	2	JE0247	Ig lambda chain NI
68	323.5	55.3	112	1	L2HUNG	Ig lambda chain V-
69	323	55.2	111	1	L6HUST	Ig lambda chain V-
70	322.5	55.1	213	2	S21066	Ig lambda chain V

ALIGNMENTS

RESULT 1
S19663
Ig lambda chain V region (clone alpha-BSA3) - human
C;Species: Homo sapiens (man)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
C;Accession: S19663
R;Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter
J. Mol. Biol. 222, 581-597, 1991
A;Title: By-passing immunization. Human antibodies from V-gene libraries displayed on pl
A;Reference number: S19663; MUID:92085276; PMID:1748994
A;Accession: S19663
A;Molecule type: mRNA
A;Residues: 1-109 <MAR>
A;Cross-references: EMBL:X61640; NID:g29492; PIDN:CAA43821.1; PID:g1340166
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-89/Domain: immunoglobulin homology <IMM>

Query Match 95.0%; Score 556; DB 2; Length 109;
Best Local Similarity 97.2%; Pred. No. 4e-41;
Matches 106; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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Qy          3 SSELTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIPDR 62
              |||||||||||||||||||:||||||||||||||||||||||||||||||||||||||||
Db          1 SSELTQDPAVSVALGQTVRITCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIPDR 60

Qy         63 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 111
```

```
                     ||||||||||||||||||||||||||||||||||||||| ||||||:|||||
Db          61 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVVFGGGTKLTVLG 109


RESULT 2
S38498
Ig lambda chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Accession: S38498
R;Marks, J.D.; Ouwehand, W.H.; Bye, J.M.; Finnern, R.; Gorick, B.D.; Voak, D.; Thorpe, S
submitted to the EMBL Data Library, June 1993
A;Description: Human antibody fragments specific for human blood group antigens from a p
A;Reference number: S38488
A;Accession: S38498
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-108 <MAR>
A;Cross-references: EMBL:Z23035; NID:g414043; PIDN:CAA80570.1; PID:g414044
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;14-88/Domain: immunoglobulin homology <IMM>

  Query Match             94.0%;  Score 550;  DB 2;  Length 108;
  Best Local Similarity   96.3%;  Pred. No. 1.3e-40;
  Matches  104;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy           4 SELTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIPDRF 63
                 ||||||||||||||||||:||||||||||||||||||||||||||||||||||||||||
Db           1 SELTQDPAVSVALGQTVRITCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIPDRF 60

Qy          64 SGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 111
                 |||||||||||||||||||||||||||||| || |||||||:|||||
Db          61 SGSSSGNTASLTITGAQAEDEADYYCNSRDSIGNGWVFGGGTKLTVLG 108


RESULT 3
S47184
Ig lambda chain - human
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Accession: S47184
R;McIntosh, R.S.; Tandon, N.; Metcalfe, R.A.; Weetman, A.P.
submitted to the EMBL Data Library, June 1994
A;Description: Cloning and analysis of IgM anti-thyroglobulin autoantibodies from patien
A;Reference number: S47181
A;Accession: S47184
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-108 <MCI>
A;Cross-references: EMBL:X79783; NID:g506426; PIDN:CAA56179.1; PID:g506427
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-89/Domain: immunoglobulin homology <IMM>

  Query Match             94.0%;  Score 550;  DB 2;  Length 108;
  Best Local Similarity   97.2%;  Pred. No. 1.3e-40;
  Matches  105;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy           3 SSELTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIPDR 62
                 ||||||||||||||||||:||||||||||||||||||||||||||||||||||||||||
Db           1 SSELTQDPAVSVALGQTVRITCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIPDR 60

Qy          63 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVL 110
                 |||||||||||||||||||||||||||||||||| ||||||:|||||
Db          61 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVVFGGGTKLTVL 108


RESULT 4
S70444
Ig lambda chain precursor V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 21-Jan-2000
C;Accession: S70444; S70426
R;Cuisinier, A.M.; Fumoux, F.; Fougereau, M.; Tonnelle, C.
Mol. Immunol. 29, 1363-1373, 1992
A;Title: IgM kappa/lambda EBV human B cell clone: an early step of differentiation of fe
A;Reference number: S70442; MUID:93024508; PMID:1383695
A;Accession: S70444
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-127 <CUI>
A;Experimental source: clone E29.1
R;Tonnelle, C.
submitted to the EMBL Data Library, May 1990
A;Reference number: S70426
A;Accession: S70426
A;Molecule type: mRNA
A;Residues: 1-90 <TON>
A;Cross-references: EMBL:X53070
A;Experimental source: cell line E29.1, clone VL 29-1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-127/Product: Ig lambda chain V region (fragment) #status predicted <MAT>
F;34-108/Domain: immunoglobulin homology <IMM>

  Query Match             93.0%;  Score 544;  DB 2;  Length 127;
  Best Local Similarity   95.4%;  Pred. No. 5e-40;
  Matches  103;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy           3 SSELTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIPDR 62
                 ||||||||||||||||||:||||||||||||||||||||||||||||||||||||||||
Db          20 SSELTQDPAVSVALGQTVRITCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIPDR 79

Qy          63 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVL 110
                 ||||||||||||||||||||||||||||||||||:||| ||::|||
Db          80 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHYVFGTGTKVTVL 127


RESULT 5
S36272
Ig lambda chain V region (clone alpha-THY-29) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
C;Accession: S36272
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
EMBO J. 12, 725-734, 1993
A;Title: Human anti-self antibodies with high specificity from phage display libraries.
A;Reference number: S36256; MUID:93178448; PMID:7679990
A;Accession: S36272
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-110 <GRI>
A;Cross-references: EMBL:Z18833; NID:g33419; PIDN:CAA79285.1; PID:g939912
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-89/Domain: immunoglobulin homology <IMM>

  Query Match             92.2%;  Score 539.5;  DB 2;  Length 110;
  Best Local Similarity   95.5%;  Pred. No. 1.1e-39;
  Matches  105;  Conservative    3;  Mismatches    1;  Indels    1;  Gaps    1;

Qy           3 SSELTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIPDR 62
                 ||||||||||||||||||:||||||||||||||||||||||||||||||||||||||||
Db           1 SSELTQDPAVSVALGQTVRITCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIPDR 60

Qy          63 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGN-HWVFGGGTELTVLG 111
                 |||||||||||||||||||||||||||||||||| : ||||||:|||||
Db          61 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNLYVVFGGGTKLTVLG 110


RESULT 6
S38496
Ig lambda chain - human (fragment)
C;Species: Homo sapiens (man)
```

```
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Accession: S38496
R;Marks, J.D.; Ouwehand, W.H.; Bye, J.M.; Finnern, R.; Gorick, B.D.; Voak, D.; Thorpe, S
submitted to the EMBL Data Library, June 1993
A;Description: Human antibody fragments specific for human blood group antigens from a p
A;Reference number: S38488
A;Accession: S38496
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-109 <MAR>
A;Cross-references: EMBL:Z23031; NID:g414039; PIDN:CAA80566.1; PID:g414040
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-89/Domain: immunoglobulin homology <IMM>

  Query Match             90.1%;  Score 527;  DB 2;  Length 109;
  Best Local Similarity   90.8%;  Pred. No. 1.2e-38;
  Matches   99;  Conservative    6;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          3 SSELTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIPDR 62
              ||||||||||||||||||:|||||||:||||||||||||||||||:||||||||||||||
Db          1 SSELTQDPAVSVALGQTVRITCQGDSLKSYYASWYQQKPGQAPVLVMYGKNNRPSGIPDR 60

Qy         63 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 111
              ||||  |||||||||||||||||||| |||:|||| :|||||:|||||
Db         61 FSGSYPGNTASLTITGAQAEDEADYYCTSRDTSGNHVLFGGGTKLTVLG 109


RESULT 7
S25748
Ig lambda chain - human
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S25748
R;Combriato, G.; Klobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A;Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam
A;Reference number: S16439; MUID:91257162; PMID:1904362
A;Accession: S25748
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-233 <COM>
A;Cross-references: EMBL:X57813; NID:g33725; PIDN:CAA40950.1; PID:g33726
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;148-216/Domain: immunoglobulin homology <IMM>

  Query Match             88.5%;  Score 518;  DB 2;  Length 233;
  Best Local Similarity   89.0%;  Pred. No. 1.6e-37;
  Matches   97;  Conservative    7;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          3 SSELTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIPDR 62
              ||||||||||||||||||:|||||||:||||||| ||||||:|||||:||||||||||
Db         20 SSELTQDPAVSVALGQTVRITCQGDSLRAYYASWYQHKPGQAPILVIYGENNRPSGIPDR 79

Qy         63 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 111
              ||||||||||  ||||||||||||||||||:  :|||||:|||||
Db         80 FSGSSSGNTASFAITGAQAEDEADYYCNSRDSSGDQVLFGGGTKLTVLG 128


RESULT 8
L3HUSH
Ig lambda chain V-III region (Sh) - human
C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 02-Sep-1997
C;Accession: A01980
R;Titani, K.; Wikler, M.; Shinoda, T.; Putnam, F.W.
J. Biol. Chem. 245, 2171-2176, 1970
A;Title: The amino acid sequence of a lambda type Bence-Jones protein. III. The complete
A;Reference number: A92057; MUID:70166723; PMID:4909564
A;Accession: A01980
A;Molecule type: protein
A;Residues: 1-108 <TIT>
A;Note: the sequence of the C region is also given
C;Genetics:
A;Gene: GDB:IGLV@
A;Cross-references: GDB:119342; OMIM:147240
A;Map position: 22q11.2-22q11.2
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into l
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;14-88/Domain: immunoglobulin homology <IMM>
F;21-86/Disulfide bonds: #status experimental

  Query Match             88.0%;  Score 515;  DB 1;  Length 108;
  Best Local Similarity   89.8%;  Pred. No. 1.3e-37;
  Matches   97;  Conservative    7;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          4 SELTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIPDRF 63
              ||||||||||||||||||:|||||||  | |:||||||||||:|||||:||||||||||
Db          1 SELTQDPAVSVALGQTVRITCQGDSLRGYDAAWYQQKPGQAPLLVIYGRNNRPSGIPDRF 60

Qy         64 SGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 111
              ||||||:|||||||||||||||||||||||| | :|||||:|||||
Db         61 SGSSSGHTASLTITGAQAEDEADYYCNSRDSSGKHVLFGGGTKLTVLG 108


RESULT 9
S19672
Ig lambda chain V region (clone alpha-TEL14) - human
C;Species: Homo sapiens (man)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
C;Accession: S19672
R;Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter
J. Mol. Biol. 222, 581-597, 1991
A;Title: By-passing immunization. Human antibodies from V-gene libraries displayed on pl
A;Reference number: S19663; MUID:92085276; PMID:1748994
A;Accession: S19672
A;Molecule type: mRNA
A;Residues: 1-110 <MAR>
A;Cross-references: EMBL:X61644; NID:g37856; PIDN:CAA43825.1; PID:g1335384
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-89/Domain: immunoglobulin homology <IMM>

  Query Match             87.3%;  Score 510.5;  DB 2;  Length 110;
  Best Local Similarity   90.0%;  Pred. No. 3.3e-37;
  Matches   99;  Conservative    5;  Mismatches    5;  Indels    1;  Gaps    1;

Qy          3 SSELTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIPDR 62
              |||||||||||||| |||||:||||||||| ||||||||||||:|||||:|:|||||||
Db          1 SSELTQDPAVSVAFGQTVRITCQGDSLRSSYASWYQQKPGQAPLLVIYGENSRPSGIPDR 60

Qy         63 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHW-VFGGGTELTVLG 111
              |||||||||||||||||||||||||||||||||||||| | |  ||||||:|||||
Db         61 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSRGTHLEVFGGGTKLTVLG 110


RESULT 10
S02083
Ig lambda chain V-IV region - human (tentative sequence) (fragments)
N;Alternate names: amyloid-fibril protein GIL
C;Species: Homo sapiens (man)
C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 31-Mar-2000
C;Accession: S02083
R;Fykse, E.M.; Sletten, K.; Husby, G.; Cornwell III, G.G.
Biochem. J. 256, 973-980, 1988
A;Title: The primary structure of the variable region of an immunoglobulin IV light-cha
A;Reference number: S02083; MUID:89134210; PMID:3146981
A;Accession: S02083
A;Molecule type: protein
A;Residues: 1-70;71-72;73-75;76-131;132-146 <FYK>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;14-88/Domain: immunoglobulin homology <IMM>
```

```
  Query Match             86.4%;  Score 505.5;  DB 2;  Length 146;
  Best Local Similarity   88.9%;  Pred. No. 1.2e-36;
  Matches   96;  Conservative    9;  Mismatches    2;  Indels    1;  Gaps    1;

Qy          4 SELTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIPDRF 63
              |||||||||||||||||:||||||||:: ||||||||||||:|||||||||||||||:||
Db          1 SELTQDPAVSVALGQTVRITCQGDSLRNFVASWYQQKPGQAPLLVIYGKNNRPSGIPBRF 60

Qy         64 SGSSSGNTASLTITGAQAEDEADYYCNSRDSSGN-HWVFGGGTELTVL 110
              |||||||||||||||:||||||||||||:|||| | :|||||:||||
Db         61 SGSSSGNTASLTITGARAEDEADYYCNSRNSSGNYHVIFGGGTKLTVL 108


RESULT 11
S36060
Ig lambda chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 21-Jan-2000
C;Accession: S36060
[redacted]illiams, S.C.
Submitted to the EMBL Data Library, April 1993
A;Reference number: S36046
A;Accession: S36060
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-96 <WIL>
A;Cross-references: EMBL:Z22202; NID:g312325; PIDN:CAA80211.1; PID:g312326
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-89/Domain: immunoglobulin homology <IMM>

  Query Match             85.8%;  Score 502;  DB 2;  Length 96;
  Best Local Similarity   99.0%;  Pred. No. 1.5e-36;
  Matches   95;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 SSELTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIPDR 62
              |||||||||||||||||:||||||||||||||||||||||||||||||||||||||||||
Db          1 SSELTQDPAVSVALGQTVRITCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIPDR 60

Qy         63 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNH 98
              ||||||||||||||||||||||||||||||||||||
Db         61 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNH 96


RESULT 12
S13726
[redacted]ambda chain V region - human
[redacted]ecies: Homo sapiens (man)
C;Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S13726
R;Frippiat, J.P.; Chuchana, P.; Bernard, F.; Buluwela, L.; Lefranc, G.; Lefranc, M.P.
Nucleic Acids Res. 18, 7134, 1990
A;Title: First genomic sequence of a human Ig variable lambda gene belonging to subgroup
A;Reference number: S13726; MUID:91088295; PMID:2124677
A;Accession: S13726
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-115 <FRI>
A;Cross-references: EMBL:X56178; NID:g33404; PIDN:CAA39639.1; PID:g33405
C;Genetics:
A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-108/Domain: immunoglobulin homology <IMM>

  Query Match             85.8%;  Score 502;  DB 2;  Length 115;
  Best Local Similarity   99.0%;  Pred. No. 1.8e-36;
  Matches   95;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 SSELTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIPDR 62
              |||||||||||||||||:||||||||||||||||||||||||||||||||||||||||||
Db         20 SSELTQDPAVSVALGQTVRITCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIPDR 79

Qy         63 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNH 98
              ||||||||||||||||||||||||||||||||||||
Db         80 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNH 115


RESULT 13
S25741
Ig lambda chain - human
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S25741
R;Combriato, G.; Klobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A;Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam
A;Reference number: S16439; MUID:91257162; PMID:1904362
A;Accession: S25741
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-233 <COM>
A;Cross-references: EMBL:X57805; NID:g33707; PIDN:CAA40943.1; PID:g33708
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;148-216/Domain: immunoglobulin homology <IMM>

  Query Match             84.4%;  Score 494;  DB 2;  Length 233;
  Best Local Similarity   85.2%;  Pred. No. 1.8e-35;
  Matches   92;  Conservative    9;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          3 SSELTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIPDR 62
              |||||||| |||||||||:|: ||||::||||||||||||||||| |:| ||:|||||||||
Db         20 SSELTQDPTVSVALGQTLRIKCQGDTIRSYYASWYQQKPGQAPTLLINGKDNRPSGIPDR 79

Qy         63 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVL 110
              ||||:|||||||||||| |||||||||||||||| :| ||||||:||||
Db         80 FSGSTSGNTASLTITGTQAEDEADYYCNSRDSSAHHLVFGGGTKLTVL 127


RESULT 14
S38495
Ig lambda chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Accession: S38495
R;Marks, J.D.; Ouwehand, W.H.; Bye, J.M.; Finnern, R.; Gorick, B.D.; Voak, D.; Thorpe, S
submitted to the EMBL Data Library, June 1993
A;Description: Human antibody fragments specific for human blood group antigens from a p
A;Reference number: S38488
A;Accession: S38495
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-106 <MAR>
A;Cross-references: EMBL:Z23029; NID:g414037; PIDN:CAA80564.1; PID:g414038
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-89/Domain: immunoglobulin homology <IMM>

  Query Match             73.6%;  Score 430.5;  DB 2;  Length 106;
  Best Local Similarity   76.1%;  Pred. No. 2.4e-30;
  Matches   83;  Conservative   13;  Mismatches   10;  Indels    3;  Gaps    1;

Qy          3 SSELTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIPDR 62
              |||||||||||||||||:|||||||||||||||||||:||||::  | ||||||:|
Db          1 SSELTQDPAVSVALGQTVRITCQGDSLRSYYASWYQQKPGQSPVLVMFLDNKRPSGIPER 60

Qy         63 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 111
              ||||:|||||:|||:  || |||||:| : |   |  :|||||::||||
Db         61 FSGSNSGNTATLTISETQAMDEADYFCQAWD---NGVIFGGGTKVTVLG 106


RESULT 15
S49533
anti-Sm antibody VL chain (V lambda 3b/J lambda 2/3) - human
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C;Species: Homo sapiens (man)
C;Date: 01-Feb-1995 #sequence_revision 12-May-1995 #text_change 21-Jan-2000
C;Accession: S49533
R;Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
submitted to the EMBL Data Library, October 1994
A;Description: Molecular characterization of natural human anti-Sm autoantibodies.
A;Reference number: S48797
A;Accession: S49533
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-105 <MAH>
A;Cross-references: EMBL:Z46346; NID:g560845; PIDN:CAA86465.1; PID:g1340169
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;11-85/Domain: immunoglobulin homology <IMM>

  Query Match            69.7%;  Score 408;  DB 2;  Length 105;
  Best Local Similarity  73.3%;  Pred. No. 2e-28;
  Matches   77;  Conservative   10;  Mismatches   18;  Indels    0;  Gaps    0;

Qy          7 TQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIPDRFSGS 66
              || |:|||: ||| |:|| ||:|   || |||||||||||||  : ||||||:|||||
Db          1 TQPPSVSVSPGQTARITCSGDALPKQYAYWYQQKPGQAPVLVIYKDSERPSGIPERFSGS 60

Qy         67 SSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 111
              ||| | :|||:| |||||||||| | |||| : ||||||:|||||
Db         61 SSGTTVTLTISGVQAEDEADYYCQSADSSGTYVVFGGGTKLTVLG 105


Search completed: September  9, 2004, 11:07:25
Job time : 13.3333 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: September 9, 2004, 10:58:34 ; Search time 8.0641 Seconds
(without alignments)
716.730 Million cell updates/sec

Title: US-09-880-748-2_COPY_139_249
Perfect score: 585
Sequence: 1 AFSSELTQDPAVSVALGQTV.....RDSSGNHWVFGGGTELTVLG 111

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 70 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	515	88.0	108	1	LV3A_HUMAN	P01714 homo sapien
2	367	62.7	107	1	LV4C_HUMAN	P01717 homo sapien
3	365	62.4	111	1	LV3B_HUMAN	P80748 homo sapien
4	358	61.2	108	1	LV5A_HUMAN	P01719 homo sapien
5	357	61.0	106	1	LV4A_HUMAN	P01715 homo sapien
6	350	59.8	106	1	LV4E_HUMAN	P06889 homo sapien
7	348	59.5	106	1	LV4B_HUMAN	P01716 homo sapien
8	344	58.8	130	1	LV1G_HUMAN	P06316 homo sapien
9	339	57.9	111	1	LV2F_HUMAN	P01709 homo sapien
10	333	56.9	106	1	LV4D_HUMAN	P01718 homo sapien
11	330	56.4	111	1	LV2C_HUMAN	P01706 homo sapien
12	327	55.9	111	1	LV1D_HUMAN	P01702 homo sapien
13	325	55.6	111	1	LV2H_HUMAN	P01711 homo sapien
14	323.5	55.3	112	1	LV2K_HUMAN	P04209 homo sapien
15	323	55.2	111	1	LV6C_HUMAN	P06317 homo sapien
16	322	55.0	111	1	LV2G_HUMAN	P01710 homo sapien
17	319	54.5	111	1	LV7A_HUMAN	P01720 homo sapien
18	315	53.8	109	1	LV1F_HUMAN	P04208 homo sapien
19	310	53.0	111	1	LV1C_HUMAN	P01701 homo sapien
20	309.5	52.9	112	1	LV6A_HUMAN	P01721 homo sapien
21	308	52.6	109	1	LV2E_HUMAN	P01708 homo sapien
22	308	52.6	111	1	LV2I_HUMAN	P01712 homo sapien
23	306.5	52.4	131	1	LV6E_HUMAN	P06319 homo sapien
24	303	51.8	111	1	LV2A_HUMAN	P01704 homo sapien
25	300	51.3	109	1	LV1I_HUMAN	P06888 homo sapien
26	298.5	51.0	110	1	LV2J_HUMAN	P01713 homo sapien
27	297	50.8	111	1	LV6D_HUMAN	P06318 homo sapien
28	296	50.6	111	1	LV2B_HUMAN	P01705 homo sapien
29	293.5	50.2	112	1	LV6B_HUMAN	P01722 homo sapien
30	293	50.1	111	1	LV2D_HUMAN	P01707 homo sapien
31	292	49.9	113	1	LV1_CHICK	P04210 gallus gall
32	289.5	49.5	112	1	LV1B_HUMAN	P01700 homo sapien
33	288.5	49.3	112	1	LV1H_HUMAN	P06887 homo sapien
34	280	47.9	111	1	LV1A_HUMAN	P01699 homo sapien
35	279.5	47.8	129	1	LV1B_MOUSE	P01724 mus musculu
36	274.5	46.9	110	1	KV13_RABIT	P01694 oryctolagus
37	267.5	45.7	129	1	LV1D_MOUSE	P01726 mus musculu
38	267.5	45.7	129	1	LV1E_MOUSE	P01727 mus musculu
39	265.5	45.4	110	1	LV1C_MOUSE	P01725 mus musculu
40	261	44.6	111	1	LV2L_HUMAN	P80422 homo sapien
41	261	44.6	117	1	KV10_RABIT	P01691 oryctolagus
42	254	43.4	103	1	LV1E_HUMAN	P01703 homo sapien
43	251.5	43.0	136	1	KV5B_MOUSE	P01634 mus musculu
44	247.5	42.3	108	1	KV1M_HUMAN	P01605 homo sapien
45	245	41.9	110	1	KV3P_MOUSE	P01668 mus musculu
46	244.5	41.8	110	1	KV01_RABIT	P01682 oryctolagus
47	244	41.7	129	1	KV3M_HUMAN	P18136 homo sapien
48	243.5	41.6	111	1	KV3O_MOUSE	P01667 mus musculu
49	243	41.5	133	1	KV4B_HUMAN	P06313 homo sapien
50	242.5	41.5	109	1	KV14_RABIT	P01695 oryctolagus
51	241.5	41.3	108	1	KV07_RABIT	P01688 oryctolagus
52	241.5	41.3	131	1	KV3I_MOUSE	P01661 mus musculu
53	241	41.2	108	1	KV6K_MOUSE	P04945 mus musculu
54	239.5	40.9	108	1	KV1B_HUMAN	P01594 homo sapien
55	239.5	40.9	110	1	KV15_RABIT	P01696 oryctolagus
56	239.5	40.9	111	1	KV3L_MOUSE	P01664 mus musculu
57	239	40.9	109	1	KV3E_HUMAN	P01623 homo sapien
58	238.5	40.8	111	1	KV3E_MOUSE	P01657 mus musculu
59	238.5	40.8	111	1	KV3H_MOUSE	P01660 mus musculu
60	238.5	40.8	111	1	KV3Q_MOUSE	P01669 mus musculu
61	238.5	40.8	129	1	LV2B_MOUSE	P01729 mus musculu
62	237.5	40.6	134	1	KV4C_HUMAN	P06314 homo sapien
63	236.5	40.4	108	1	KV1H_HUMAN	P01600 homo sapien
64	236.5	40.4	109	1	KV03_RABIT	P01684 oryctolagus
65	236	40.3	129	1	KV3L_HUMAN	P18135 homo sapien
66	235.5	40.3	111	1	KV3M_MOUSE	P01665 mus musculu
67	235.5	40.3	114	1	KV4A_HUMAN	P01625 homo sapien
68	234.5	40.1	108	1	KV08_RABIT	P01689 oryctolagus
69	234.5	40.1	115	1	KV02_RABIT	P01683 oryctolagus
70	234	40.0	107	1	KV6A_MOUSE	P01675 mus musculu

ALIGNMENTS

RESULT 1
LV3A_HUMAN
ID LV3A_HUMAN STANDARD; PRT; 108 AA.
AC P01714;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig lambda chain V-III region SH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=70166723; PubMed=4909564;
RA Titani K., Wikler M., Shinoda T., Putnam F.W.;
RT "The amino acid sequence of a lambda type Bence-Jones protein. 3. The
RT complete amino acid sequence and the location of the disulfide
RT bridges.";
RL J. Biol. Chem. 245:2171-2176(1970).
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A01980; L3HUSH.
DR HSSP; P80748; 2LOI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGv; 1.

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DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Bence-Jones protein.
FT   DOMAIN        1     97       IG-LIKE.
FT   DISULFID     21     86
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11392 MW;  E7E1229586411A56 CRC64;

  Query Match             88.0%;  Score 515;  DB 1;  Length 108;
  Best Local Similarity   89.8%;  Pred. No. 1.8e-44;
  Matches   97;  Conservative    7;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          4 SELTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIPDRF 63
              ||||||||||||||||||:||||||| | |:||||||||||:|||||:||||||||||||
Db          1 SELTQDPAVSVALGQTVRITCQGDSLRGYDAAWYQQKPGQAPLLVIYGRNNRPSGIPDRF 60

Qy         64 SGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 111
              ||||||:|||||||||||||||||||||||| | :|||||:|||||
Db         61 SGSSSGHTASLTITGAQAEDEADYYCNSRDSSGKHVLFGGGTKLTVLG 108


RESULT 2
LV4C_HUMAN
ID   LV4C_HUMAN     STANDARD;      PRT;   107 AA.
AC   P01717;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig lambda chain V-IV region Hil.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=78187276; PubMed=418804;
RA   Lopez de Castro J.A., Chiu Y.-Y.H., Poljak R.J.;
RT   "Amino acid sequence of the variable region of the light (lambda)
RT   chain from human myeloma cryoimmunoglobulin IgG Hil.";
RL   Biochemistry 17:1718-1723(1978).
CC   -!- MISCELLANEOUS: THE SEQUENCE OF THE C REGION IS APPARENTLY
CC       IDENTICAL WITH THAT OF HUMAN SH LAMBDA CHAIN EXCEPT IN HAVING
CC       155-ILE (HIL NUMBERING) INSTEAD OF VAL.
CC   -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A01983; L4HUHL.
DR   HSSP; P80748; 2LOI.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region.
FT   DOMAIN        1     97       IG-LIKE.
FT   NON_TER     107    107
SQ   SEQUENCE   107 AA;  11517 MW;  A5C8AFFE0C0C590A CRC64;

  Query Match             62.7%;  Score 367;  DB 1;  Length 107;
  Best Local Similarity   64.2%;  Pred. No. 8.8e-30;
  Matches   70;  Conservative   16;  Mismatches   21;  Indels    2;  Gaps    1;

Qy          3 SSELTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIPDR 62
              | |||| |:|||: ||| |:||  ::| : || |||||||:|||:|||    |||||| |
Db          1 SYELTQPPSVSVSPGQTARITCSANALPNQYAYWYQQKPGRAPVMVIYKDTQRPSGIPQR 60

Qy         63 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 111
              || |:|| | :|||:| |||||||||| : |:| :  :|||||:|||||
Db         61 FSSSTSGTTVTLTISGVQAEDEADYYCQAWDNSAS--IFGGGTKLTVLG 107


RESULT 3
LV3B_HUMAN
ID   LV3B_HUMAN     STANDARD;      PRT;   111 AA.
AC   P80748;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig lambda chain V-III region LOI.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE, SUBUNIT, DISEASE, AND 3D-STRUCTURE MODELLING.
RC   TISSUE=Urine;
RX   MEDLINE=99441384; PubMed=10510403;
RA   Jokiranta T.S., Solomon A., Pangburn M.K., Zipfel P.F., Meri S.;
RT   "Nephritogenic lambda light chain dimer: a unique human
RT   miniautoantibody against complement factor H.";
RL   J. Immunol. 163:4590-4596(1999).
CC   -!- FUNCTION: ACTIVATES THE ALTERNATIVE COMPLEMENT PATHWAY BY BINDING
CC       TO THE SHORT CONSENSUS REPEAT DOMAIN 3 (SCR3) OF FACTOR H.
CC   -!- SUBUNIT: Homodimer.
CC   -!- DISEASE: The blocking of factor H by LOI protein leads to the
CC       developmental of membranoproliferative glomerulonephritis (MPGN).
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PDB; 2LOI; 29-DEC-99.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; 3D-structure.
FT   DOMAIN        1     97       IG-LIKE.
FT   BINDING      15     15       SCR3.
FT   BINDING      25     25       SCR3.
FT   BINDING      29     29       SCR3.
FT   BINDING      48     51       SCR3.
FT   BINDING      94     94       SCR3.
FT   DISULFID     21     86       BY SIMILARITY.
FT   STRAND        4      4
FT   STRAND        8      8
FT   TURN         13     14
FT   STRAND       16     22
FT   STRAND       32     37
FT   TURN         38     40
FT   STRAND       41     46
FT   TURN         49     50
FT   STRAND       54     54
FT   TURN         55     55
FT   TURN         58     59
FT   STRAND       60     61
FT   STRAND       64     65
FT   TURN         66     67
FT   STRAND       68     74
FT   TURN         78     79
FT   STRAND       82     88
FT   TURN         91     93
FT   STRAND       97     98
FT   STRAND      102    104
FT   TURN        107    108
FT   NON_TER     111    111
SQ   SEQUENCE   111 AA;  11935 MW;  69498EBEFDE82053 CRC64;

  Query Match             62.4%;  Score 365;  DB 1;  Length 111;
  Best Local Similarity   67.6%;  Pred. No. 1.5e-29;
  Matches   71;  Conservative   12;  Mismatches   22;  Indels    0;  Gaps    0;

Qy          6 LTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIPDRFSG 65
              ||| |:|||| |:| |:|| |: : |    ||||||||||||||   :||||||:||||
Db          3 LTQPPSVSVAPGETARLTCGGNDIGSESVHWYQQKPGQAPVLVIYFDRDRPSGIPERFSG 62
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Qy          66 SSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVL 110
               |:|||||:|||:  :| |||||||   |||  | ||||||:||||
Db          63 SNSGNTATLTISRVEAGDEADYYCQLWDSSSEHVVFGGGTKLTVL 107


RESULT 4
LV5A_HUMAN
ID   LV5A_HUMAN     STANDARD;      PRT;   108 AA.
AC   P01719;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig lambda chain V-V region DEL.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=75112179; PubMed=4452363;
RA   Eulitz M.;
RT   "A new subgroup of human L-chains of the lambda-type. Primary
RT   structure of Bence-Jones protein DEL.";
RL   Eur. J. Biochem. 50:49-69(1974).
CC   -!- MISCELLANEOUS: THIS IS THE FIRST SEQUENCED V REGION OF LAMBDA
CC       CHAIN SUBGROUP V.
CC   -!- MISCELLANEOUS: This is a Bence-Jones protein.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A01985; L5HUDL.
DR   HSSP; P80748; 2LOI.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Bence-Jones protein.
FT   DOMAIN        1     97       IG-LIKE.
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11342 MW;  B8E8ED9C09C9E451 CRC64;

  Query Match             61.2%;  Score 358;  DB 1;  Length 108;
  Best Local Similarity   64.2%;  Pred. No. 7e-29;
  Matches   68;  Conservative   14;  Mismatches   24;  Indels    0;  Gaps    0;

Qy           6 LTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIPDRFSG 65
               |:| |:|||| ||| |:|| || :      ||||||||||||::  |:||:|||:||||
Db           3 LSQPPSVSVAPGQTARITCGGDGIGGKSVHWYQQKPGQAPVLVVHEDNDRPAGIPERFSG 62

Qy          66 SSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 111
               |:|||||:|||:  :| |||||||   |    | ||||||:|||||
Db          63 SNSGNTAALTISRVEAGDEADYYCEVWDDRTAHVVFGGGTKLTVLG 108


RESULT 5
LV4A_HUMAN
ID   LV4A_HUMAN     STANDARD;      PRT;   106 AA.
AC   P01715;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig lambda chain V-IV region Bau.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=75059189; PubMed=4435717;
RA   Baczko K., Braun D., Hilschmann N.;
RT   "Pattern of antibody structure, the primary structure of monoclonal
RT   immunoglobulin L-chain of the lambda-type, subgroup IV (Bence-Jones
RT   protein Bau.).";
RL   Hoppe-Seyler's Z. Physiol. Chem. 355:131-154(1974).
CC   -!- MISCELLANEOUS: This is a Bence-Jones protein.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A01981; L4HUBU.
DR   HSSP; P80748; 2LOI.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Bence-Jones protein.
FT   DOMAIN        1     102       IG-LIKE.
FT   NON_TER     106     106
SQ   SEQUENCE   106 AA;  11305 MW;  4B6A688E0EC46571 CRC64;

  Query Match             61.0%;  Score 357;  DB 1;  Length 106;
  Best Local Similarity   65.1%;  Pred. No. 8.6e-29;
  Matches   69;  Conservative   13;  Mismatches   22;  Indels    2;  Gaps    1;

Qy           6 LTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIPDRFSG 65
               ||| |::||: |||  :|| || |   |  ||||||||:||||||  : ||||||:||||
Db           3 LTQPPSLSVSPGQTASITCSGDKLGEQYVCWYQQKPGQSPVLVIYHDSKRPSGIPERFSG 62

Qy          66 SSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 111
               |:|| ||:|||:| || ||||||| : ||     :|||||:|||||
Db          63 SNSGTTATLTISGTQAMDEADYYCQAWDS--YTVIFGGGTKLTVLG 106


RESULT 6
LV4E_HUMAN
ID   LV4E_HUMAN     STANDARD;      PRT;   106 AA.
AC   P06889;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig lambda chain V-IV region MOL.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=87156515; PubMed=3103603;
RA   Holm E., Sletten K., Husby G.;
RT   "Structural studies of a carbohydrate-containing
RT   immunoglobulin-lambda-light-chain amyloid-fibril protein (AL) of
RT   variable subgroup III.";
RL   Biochem. J. 239:545-551(1986).
CC   -!- MISCELLANEOUS: RESIDUES 29-30 AND 56-58 WERE POSITIONED BY
CC       HOMOLOGY.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A26019; L4HUML.
DR   HSSP; P80748; 2LOI.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Amyloid; Glycoprotein.
FT   DOMAIN        1     103       IG-LIKE.
FT   DISULFID     21      86       BY SIMILARITY.
FT   CARBOHYD     90      90       N-LINKED (GLCNAC. . .) (PROBABLE).
FT   NON_TER     106     106
SQ   SEQUENCE   106 AA;  11272 MW;  D9BB77D4797D2123 CRC64;
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  Query Match             59.8%;  Score 350;  DB 1;  Length 106;
  Best Local Similarity   62.6%;  Pred. No. 4.3e-28;
  Matches   67;  Conservative   17;  Mismatches   21;  Indels    2;  Gaps    1;

Qy          5 ELTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIPDRFS 64
              |||| |:|||: |||  ::| || |    |  |||| |||:|:|||| : |||||||:|||
Db          2 ELTQPPSVSVSPGQTATISCSGDKLGESYYDWYQQSPGQSPLLVIYEGDKRPSGIPERFS 61

Qy         65 GSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 111
              ||:|||||:|||:| :: ||||||| : :||    :|||||:|||||
Db         62 GSNSGNTATLTISGTESMDEADYYCQAWNSSS--VLFGGGTKLTVLG 106


RESULT 7
LV4B_HUMAN
ID   LV4B_HUMAN     STANDARD;      PRT;   106 AA.
AC   P01716;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig lambda chain V-IV region X.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=69088380; PubMed=4883841;
RA   Milstein C., Clegg J.B., Jarvis J.M.;
RT   "Immunoglobulin lambda-chains. The complete amino acid sequence of a
RT   Bence-Jones protein.";
RL   Biochem. J. 110:631-652(1968).
CC   -!- MISCELLANEOUS: This is a Bence-Jones protein.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A01982; L4HUX.
DR   HSSP; P80748; 2LOI.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Bence-Jones protein.
FT   DOMAIN        1    102       IG-LIKE.
FT   NON_TER     106    106
SQ   SEQUENCE   106 AA;  11334 MW;  24D04344AA812855 CRC64;

  Query Match             59.5%;  Score 348;  DB 1;  Length 106;
  Best Local Similarity   65.1%;  Pred. No. 6.8e-28;
  Matches   69;  Conservative   11;  Mismatches   24;  Indels    2;  Gaps    1;

Qy          5 ELTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIPDRFS 64
              :||| |:|||: |||  :|| || |      ||||:|||:|||||| | | ||||:|||
Db          2 DLTQPPSVSVSPGQTASITCSGDKLGDKDVCWYQQRPGQSPVLVIYQDNQRSSGIPERFS 61

Qy         65 GSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVL 110
              ||:|||||:|||:| || ||||||| : ||     |||||| ||||
Db         62 GSNSGNTATLTISGTQAMDEADYYCQAWDSMS--VVFGGGTRLTVL 105


RESULT 8
LV1G_HUMAN
ID   LV1G_HUMAN     STANDARD;      PRT;   130 AA.
AC   P06316;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig lambda chain V-I region BL2 precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85062823; PubMed=6095199;
RA   Tsujimoto Y., Croce C.M.;
RT   "Molecular cloning of a human immunoglobulin lambda chain variable
RT   sequence.";
RL   Nucleic Acids Res. 12:8407-8414(1984).
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; X01147; CAA25598.1; -.
DR   PIR; A01966; L1HUBL.
DR   HSSP; P01703; 7FAB.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    130       IG LAMBDA CHAIN V-I REGION BL2.
FT   DOMAIN       20    115       V SEGMENT.
FT   DOMAIN      116    130       J SEGMENT.
FT   DISULFID     41    108       BY SIMILARITY.
FT   NON_TER     130    130
SQ   SEQUENCE   130 AA;  13564 MW;  FA44BB17D3A55EBF CRC64;

  Query Match             58.8%;  Score 344;  DB 1;  Length 130;
  Best Local Similarity   61.8%;  Pred. No. 2.1e-27;
  Matches   68;  Conservative   13;  Mismatches   27;  Indels    2;  Gaps    1;

Qy          4 SELTQDPAVSVALGQTVRVTCQGDS--LRSYYASWYQQKPGQAPVLVIYGKNNRPSGIPD 61
              | ||| |:|| | || | ::| | |  : : | ||||| || || |:||  | |||||||
Db         21 SVLTQPPSVSAAPGQKVTISCSGSSSNIGNDYVSWYQQVPGTAPKLLIYDNNKRPSGIPD 80

Qy         62 RFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 111
              ||||| || :|:| ||| |  ||||||| : ::| : |||||||:|||||
Db         81 RFSGSKSGTSATLGITGLQTGDEADYYCGTWNNSLSGWVFGGGTKLTVLG 130


RESULT 9
LV2F_HUMAN
ID   LV2F_HUMAN     STANDARD;      PRT;   111 AA.
AC   P01709;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig lambda chain V-II region MGC.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=75013804; PubMed=4415202;
RA   Fett J.W., Deutsch H.F.;
RT   "Primary structure of the Mcg lambda chain.";
RL   Biochemistry 13:4102-4114(1974).
RN   [2]
RP   LAMBDA CHAIN GENES.
RX   MEDLINE=76093781; PubMed=812801;
RA   Fett J.W., Deutsch H.F.;
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RT   "A new lambda-chain gene.";
RL   Immunochemistry 12:643-652(1975).
RN   [3]
RP   X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RA   Edmundson A.B., Ely K.R., Abola E.E., Schiffer M.,
RA   Panagiotopoulos N.;
RT   "Rotational allomerism and divergent evolution of domains in
RT   immunoglobulin light chains.";
RL   Biochemistry 14:3953-3961(1975).
RN   [4]
RP   X-RAY CRYSTALLOGRAPHY.
RX   MEDLINE=90133913; PubMed=2515285;
RA   Ely K.R., Herron J.N., Harker M., Edmundson A.B.;
RT   "Three-dimensional structure of a light chain dimer crystallized in
RT   water. Conformational flexibility of a molecule in two crystal
RT   forms.";
RL   J. Mol. Biol. 210:601-615(1989).
CC   -!- MISCELLANEOUS: This is a Bence-Jones protein.
CC   -!- MISCELLANEOUS: THE MCG-TYPE C REGION APPEARS TO BE CORRELATED WITH
CC       A VERY UNUSUAL V-REGION SUBSTITUTION, 103-THR ABOVE FOR GLY,
CC       SUGGESTING THAT THE V-C JOINING MECHANISM IS NOT ALWAYS RANDOM.
CC   -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE KERN+ AND MCG+
CC       MARKERS.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A90381; L2HUMC.
DR   PDB; 2MCG; 15-JUL-92.
DR   PDB; 1A8J; 17-JUN-98.
DR   PDB; 1DCL; 15-MAY-97.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Bence-Jones protein; 3D-structure;
KW   Pyrrolidone carboxylic acid.
FT   DOMAIN        1    108       IG-LIKE.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   DISULFID     22     90       BY SIMILARITY.
FT   STRAND        5      5
FT   STRAND       10     12
FT   STRAND       18     23
FT   TURN         26     32
FT   STRAND       36     40
FT   TURN         42     43
FT   STRAND       50     51
FT   TURN         52     54
FT   STRAND       55     55
FT   TURN         62     63
FT   STRAND       66     68
FT   STRAND       72     77
FT   HELIX        82     84
FT   STRAND       86     93
FT   STRAND       99    101
FT   STRAND      105    109
FT   NON_TER     111    111
SQ   SEQUENCE   111 AA;  11558 MW;  7CC1D6E2FA3377BA CRC64;

  Query Match             57.9%;  Score 339;  DB 1;  Length 111;
  Best Local Similarity   61.3%;  Pred. No. 5.6e-27;
  Matches   68;  Conservative   17;  Mismatches   22;  Indels    4;  Gaps    3;

Qy          4 SELTQDPAVSVALGQTVRVTCQGDS--LRSY-YASWYQQKPGQAPVLVIYGKNNRPSGIP 60
              | ||| |: | :|||:| ::| | |  :  | | |||||  |:|| ::||  | ||||:|
Db          2 SALTQPPSASGSLGQSVTISCTGTSSDVGGYNYVSWYQQHAGKAPKVIIYEVNKRPSGVP 61

Qy         61 DRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 111
              |||||| ||||||||::| ||||||||||:| : | | :||| ||::||||
Db         62 DRFSGSKSGNTASLTVSGLQAEDEADYYCSSYEGSDN-FVFGTGTKVTVLG 111
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RESULT 10
LV4D_HUMAN
ID   LV4D_HUMAN     STANDARD;      PRT;   106 AA.
AC   P01718;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig lambda chain V-IV region Kern.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=71150336; PubMed=5549568;
RA   Ponstingl H., Hess M., Hilschmann N.;
RT   "Structural rule of antibodies. Primary structure of a monoclonal
RT   immunoglobulin-L-chain of the lambda type, subgroup IV (Bence-Jones-
RT   protein Kern). V. The complete amino acid sequence and its genetic
RT   interpretation.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 352:247-266(1971).
CC   -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE KERN+ MARKER.
CC   -!- MISCELLANEOUS: This is a Bence-Jones protein.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A01984; L4HUKN.
DR   HSSP; P80748; 2LOI.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Bence-Jones protein.
FT   DOMAIN        1    102       IG-LIKE.
FT   DISULFID     21     86       BY SIMILARITY.
FT   NON_TER     106    106
SQ   SEQUENCE   106 AA;  11277 MW;  C8B4A05B9CB43CBE CRC64;

  Query Match             56.9%;  Score 333;  DB 1;  Length 106;
  Best Local Similarity   61.0%;  Pred. No. 2.1e-26;
  Matches   64;  Conservative   19;  Mismatches   20;  Indels    2;  Gaps    1;

Qy          6 LTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIPDRFSG 65
              ||| |:|||: ||| :|| ||:|   : ||:||:|||:|:|||| : ||| ||:||||
Db          3 LTQPPSVSVSPGQTAVITCSGDNLEKTFVSWFQQRPGQSPLLVIYHTSERPSEIPERFSG 62

Qy         66 SSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVL 110
              |||| ||:|||:|||: |||||:| : |:     :|||||:||||
Db         63 SSSGATATLTISGAQSVDEADYFCQTWDTITA--IFGGGTKLTVL 105


RESULT 11
LV2C_HUMAN
ID   LV2C_HUMAN     STANDARD;      PRT;   111 AA.
AC   P01706;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig lambda chain V-II region BOH.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=75115478; PubMed=804002;
RA   Kohler H., Rudofsky S., Kluskens L.;
RT   "The primary structure of a human lambda II chain.";
RL   J. Immunol. 114:415-421(1975).
CC   -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE OZ+ MARKER.
CC   -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
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CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A01972; L2HUBH.
DR   HSSP; P01709; 2MCG.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Pyrrolidone carboxylic acid.
FT   DOMAIN        1    106       IG-LIKE.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   DISULFID     22     90       BY SIMILARITY.
FT   NON_TER     111    111
SQ   SEQUENCE   111 AA;  11650 MW;  94520309932623E8 CRC64;

  Query Match             56.4%;  Score 330;  DB 1;  Length 111;
  Best Local Similarity   61.6%;  Pred. No. 4.4e-26;
  Matches   69;  Conservative   13;  Mismatches   24;  Indels    6;  Gaps    3;

Qy          4 SELTQDPAVSVALGQTVRVTCQGDSL---RSYYASWYQQKPGQAPVLVIYGKNNRPSGIP 60
              | |||  :|| : ||:| ::| | |     ::: ||||| ||:|| |:||| | ||||:|
Db          2 SALTQPRSVSGSPGQSVTISCAGTSSDVGGNHFVSWYQQHPGKAPKLIIYGVNKRPSGVP 61

Qy         61 DRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNH-WVFGGGTELTVLG 111
              ||||| ||||||||:| |||||| ||| |   :|   ||||||| |||||
Db         62 YRFSGSKSGNTASLTISGLQAEDEAHYYCCS--YAGRFTWVFGGGTNLTVLG 111


RESULT 12
LV1D_HUMAN
ID   LV1D_HUMAN     STANDARD;      PRT;   111 AA.
AC   P01702;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig lambda chain V-I region NIG-64.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=83186114; PubMed=6404900;
RA   Kametani F., Takayasu T., Suzuki S., Shinoda T., Okuyama T.,
RA   Shimizu A.;
RT   "Comparative studies on the structure of the light chains of human
RT   immunoglobulins. IV. Assignment of a subsubgroup.";
RL   J. Biochem. 93:421-429(1983).
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A01965; L1HUNG.
DR   HSSP; P01703; 7FAB.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Pyrrolidone carboxylic acid.
FT   DOMAIN        1    105       IG-LIKE.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   DISULFID     22     89       BY SIMILARITY.
FT   NON_TER     111    111
SQ   SEQUENCE   111 AA;  11454 MW;  A21C6121C18A61E0 CRC64;

  Query Match             55.9%;  Score 327;  DB 1;  Length 111;
  Best Local Similarity   60.0%;  Pred. No. 8.7e-26;
  Matches   66;  Conservative   12;  Mismatches   30;  Indels    2;  Gaps    1;

Qy          4 SELTQDPAVSVALGQTVRVTCQGDS--LRSYYASWYQQKPGQAPVLVIYGKNNRPSGIPD 61
              | ||| |:|| | || | ::| | |  :   : ||||| || || |:||  | |||||||
Db          2 SVLTQPPSVSAAPGQEVTISCSGSSSNIGDNFVSWYQQLPGTAPKLLIYDNNKRPSGIPD 61

Qy         62 RFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 111
              ||||| || :|:| ||| |  ||||||| : ||| :  :||||| :||||
Db         62 RFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSVGMFGGGTRVTVLG 111


RESULT 13
LV2H_HUMAN
ID   LV2H_HUMAN     STANDARD;      PRT;   111 AA.
AC   P01711;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig lambda chain V-II region VIL.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=71215142; PubMed=5087637;
RA   Ponstingl H., Hilschmann N.;
RT   "Structural rule of antibodies. Complete primary structure of a
RT   monoclonal immunoglobin L chain of the lambda type, subgroup II
RT   (Bence Jones protein VIL).";
RL   Hoppe-Seyler's Z. Physiol. Chem. 352:859-877(1971).
CC   -!- MISCELLANEOUS: This is a Bence-Jones protein.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A01977; L2HUVL.
DR   HSSP; P01709; 2MCG.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Bence-Jones protein.
FT   DOMAIN        1    100       IG-LIKE.
FT   DISULFID     22     90       BY SIMILARITY.
FT   NON_TER     111    111
SQ   SEQUENCE   111 AA;  11445 MW;  3913736B3EF367E0 CRC64;

  Query Match             55.6%;  Score 325;  DB 1;  Length 111;
  Best Local Similarity   62.2%;  Pred. No. 1.4e-25;
  Matches   69;  Conservative   13;  Mismatches   25;  Indels    4;  Gaps    3;

Qy          4 SELTQDPAVSVALGQTVRVTCQGDS--LRSY-YASWYQQKPGQAPVLVIYGKNNRPSGIP 60
              | |||  :|| :|||:: ::| | |  :  | | ||:|| || || |:|    |||||:
Db          2 SALTQPASVSGSLGQSITISCTGTSSDVGGYNYVSWFQQHPGTAPKLIISEVRNRPSGVS 61

Qy         61 DRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 111
              |||||| | |||||||:| ||||||||||:|  || |  ||||||:|||||
Db         62 DRFSGSKSANTASLTISGLQAEDEADYYCSSYTSS-NSVVFGGGTKLTVLG 111


RESULT 14
LV2K_HUMAN
ID   LV2K_HUMAN     STANDARD;      PRT;   112 AA.
AC   P04209;
DT   20-MAR-1987 (Rel. 04, Created)
DT   20-MAR-1987 (Rel. 04, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig lambda chain V-II region NIG-84.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
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RP   SEQUENCE.
RX   MEDLINE=85204383; PubMed=3922791;
RA   Tonoike H., Kametani F., Hoshi A., Shinoda T., Isobe T.;
RT   "Amino acid sequence of an amyloidogenic Bence Jones protein in
RT   myeloma-associated systemic amyloidosis.";
RL   FEBS Lett. 185:139-141(1985).
CC   -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN ISOLATED FROM AN
CC       INDIVIDUAL WITH MYELOMA-ASSOCIATED SYSTEMIC AMYLOIDOSIS.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A01971; L2HUNG.
DR   HSSP; P01709; 2MCG.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Amyloid; Bence-Jones protein.
FT   DOMAIN        1    102       IG-LIKE.
FT   DISULFID     22     90       BY SIMILARITY.
FT   NON_TER     112    112
SQ   SEQUENCE   112 AA;  11581 MW;  988FEF363AE1E4F3 CRC64;

  Query Match             55.3%;  Score 323.5;  DB 1;  Length 112;
  Best Local Similarity   58.6%;  Pred. No. 2e-25;
  Matches   65;  Conservative   19;  Mismatches   24;  Indels    3;  Gaps    2;

Qy          4 SELTQDPAVSVALGQTVRVTCQG--DSLRSY-YASWYQQKPGQAPVLVIYGKNNRPSGIP 60
              | |||  :|| : ||:: ::| |    :  | : ||||| ||:|| |:||  |:|||||
Db          2 SALTQPASVSGSPGQSITISCTGTTSDVGGYDFVSWYQQHPGKAPKLLIYDVNSRPSGIS 61

Qy         61 DRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 111
              :||||| |||||||||:| ||||||||||:|  :: :  ||||||:|:|||
Db         62 NRFSGSKSGNTASLTISGLQAEDEADYYCSSFTTTNSRAVFGGGTKLSVLG 112


RESULT 15
LV6C_HUMAN
ID   LV6C_HUMAN     STANDARD;      PRT;   111 AA.
AC   P06317;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig lambda chain V-VI region SUT.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RA   Solomon A., Kyle R.A., Frangione B.;
RT   "Light chain variable region subgroups of monoclonal immunoglobulins
RT   in amyloidosis AL.";
RL   (In) Glenner G.G., Osserman E.F., Benditt E.P., Calkins E.,
RL   Cohen A.S., Zucker-Franklin D. (eds.);
RL   Amyloidosis, pp.449-462, Plenum Press, New York (1986).
DR   PIR; A01988; L6HUST.
DR   PDB; 1CD0; 06-MAR-00.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; 3D-structure.
FT   DOMAIN        1     22       FRAMEWORK-1.
FT   DOMAIN       23     35       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       36     50       FRAMEWORK-2.
FT   DOMAIN       51     57       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       58     91       FRAMEWORK-3.
FT   DOMAIN       92    100       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN      101    111       FRAMEWORK-4.
FT   DISULFID     22     91       BY SIMILARITY.
FT   NON_TER     111    111
SQ   SEQUENCE   111 AA;  12247 MW;  0941DD547D983598 CRC64;

  Query Match             55.2%;  Score 323;  DB 1;  Length 111;
  Best Local Similarity   58.2%;  Pred. No. 2.2e-25;
  Matches   64;  Conservative   15;  Mismatches   25;  Indels    6;  Gaps    3;

Qy          6 LTQDPAVSVALGQTVRVTC--QGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIPDRF 63
              |||  :|| : |:|| ::|     ::  ||  ||||:||:||  ||:    ||||:||||
Db          4 LTQPHSVSESPGKTVIISCTRSDGTIAGYYVQWYQQRPGRAPTTVIFEDTQRPSGVPDRF 63

Qy         64 SGS--SSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 111
              |||   | |:|||||:| | ||||||||  | |   :|||||||:|||||
Db         64 SGSIDRSSNSASLTISGLQTEDEADYYCQSYDR--DHWVFGGGTKLTVLG 111


Search completed: September  9, 2004, 11:06:52
Job time : 8.0641 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: September 9, 2004, 11:01:20 ; Search time 34.1538 Seconds
(without alignments)
1025.434 Million cell updates/sec

Title: US-09-880-748-2_COPY_139_249
Perfect score: 585
Sequence: 1 AFSSELTQDPAVSVALGQTV.....RDSSGNHWVFGGGTELTVLG 111

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 70 summaries

Database : SPTREMBL_25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	544	93.0	107	4	Q9NSD6	Q9nsd6 homo sapien
2	438	74.9	233	4	Q8TBC9	Q8tbc9 homo sapien
3	427	73.0	233	4	Q8N5F4	Q8n5f4 homo sapien
4	419	71.6	81	4	Q7Z2E8	Q7z2e8 homo sapien
5	367.5	62.8	234	4	Q8N355	Q8n355 homo sapien
6	366.5	62.6	107	4	Q9UL82	Q9ul82 homo sapien
7	346	59.1	237	4	Q8WUK4	Q8wuk4 homo sapien
8	340	58.1	237	4	Q8WTU6	Q8wtu6 homo sapien
9	335.5	57.4	236	4	Q96E61	Q96e61 homo sapien
10	332.5	56.8	234	4	Q7Z2U7	Q7z2u7 homo sapien
11	323	55.2	116	4	Q96JD0	Q96jd0 homo sapien
12	322.5	55.1	112	4	Q96JD1	Q96jd1 homo sapien
13	319	54.5	110	4	Q8TE63	Q8te63 homo sapien
14	316	54.0	112	4	Q96JD2	Q96jd2 homo sapien
15	308.5	52.7	236	4	Q8NEJ1	Q8nej1 homo sapien
16	301	51.5	233	4	Q96I69	Q96i69 homo sapien
17	297	50.8	101	4	Q8IZD8	Q8izd8 homo sapien
18	275	47.0	108	4	Q96SB0	Q96sb0 homo sapien
19	270	46.2	235	11	Q99M11	Q99m11 mus musculu
20	267.5	45.7	129	11	Q8VDE2	Q8vde2 mus musculu
21	267	45.6	113	11	Q8CGS1	Q8cgs1 mus musculu
22	255.5	43.7	131	11	Q811C3	Q811c3 mus musculu
23	248.5	42.5	108	4	Q9UL77	Q9ul77 homo sapien
24	248	42.4	134	11	Q8VDD0	Q8vdd0 mus musculu
25	247.5	42.3	240	4	Q8WUK3	Q8wuk3 homo sapien
26	245	41.9	107	4	Q9UL81	Q9ul81 homo sapien
27	245	41.9	109	11	Q9ET13	Q9et13 mus musculu
28	244	41.7	109	4	Q9UL78	Q9ul78 homo sapien
29	244	41.7	235	11	Q7TMK0	Q7tmk0 mus musculu
30	243	41.5	107	4	Q96SA9	Q96sa9 homo sapien
31	237	40.5	114	11	Q8K1F1	Q8k1f1 mus musculu
32	235	40.2	112	11	Q8K1F2	Q8k1f2 mus musculu
33	233.5	39.9	109	11	Q920E6	Q920e6 mus musculu
34	233	39.8	109	4	Q9UL85	Q9ul85 homo sapien
35	232	39.7	112	11	Q8K1F3	Q8k1f3 mus musculu
36	230	39.3	239	4	Q8TCD0	Q8tcd0 homo sapien
37	229.5	39.2	108	4	Q9UL70	Q9ul70 homo sapien
38	229.5	39.2	298	11	Q9QYF0	Q9qyf0 mus musculu
39	229	39.1	101	11	Q9JL78	Q9jl78 mus musculu
40	228.5	39.1	111	11	Q811U6	Q811u6 mus musculu
41	228	39.0	109	4	Q9UL86	Q9ul86 homo sapien
42	228	39.0	112	11	Q8K1F0	Q8k1f0 mus musculu
43	227.5	38.9	111	11	Q920E9	Q920e9 mus musculu
44	226.5	38.7	234	11	Q8VCP0	Q8vcp0 mus musculu
45	226.5	38.7	237	13	Q7SZ36	Q7sz36 xenopus lae
46	226	38.6	106	5	Q9U410	Q9u410 schistosoma
47	224.5	38.4	107	11	Q9ERZ9	Q9erz9 mus musculu
48	224.5	38.4	109	6	Q9N0W5	Q9n0w5 oryctolagus
49	224.5	38.4	234	4	Q7Z473	Q7z473 homo sapien
50	223	38.1	97	11	Q9JL76	Q9jl76 mus musculu
51	223	38.1	103	11	Q9JL80	Q9jl80 mus musculu
52	222.5	38.0	108	4	Q9UL83	Q9ul83 homo sapien
53	222.5	38.0	236	4	Q7Z3Y4	Q7z3y4 homo sapien
54	221	37.8	99	11	Q9JL74	Q9jl74 mus musculu
55	220	37.6	243	11	Q7TQM2	Q7tqm2 mus musculu
56	219.5	37.5	114	4	Q9UL80	Q9ul80 homo sapien
57	219.5	37.5	236	11	Q7TS98	Q7ts98 mus musculu
58	219	37.4	238	11	Q99M37	Q99m37 mus musculu
59	217.5	37.2	214	11	Q9R1A5	Q9r1a5 mus musculu
60	217	37.1	239	11	Q8VC55	Q8vc55 mus musculu
61	216.5	37.0	230	4	Q7Z2U3	Q7z2u3 homo sapien
62	214.5	36.7	108	4	Q9UL79	Q9ul79 homo sapien
63	214.5	36.7	108	11	Q8VIJ0	Q8vij0 mus musculu
64	214	36.6	238	11	Q8VCI6	Q8vci6 mus musculu
65	213.5	36.5	236	11	Q7TMK3	Q7tmk3 mus musculu
66	211.5	36.2	233	11	Q91WS9	Q91ws9 mus musculu
67	210	35.9	235	11	Q91W12	Q91w12 mus musculu
68	206.5	35.3	104	11	Q9JL82	Q9jl82 mus musculu
69	200	34.2	248	13	Q7SYU1	Q7syu1 xenopus lae
70	199	34.0	241	11	Q921A6	Q921a6 mus musculu

ALIGNMENTS

RESULT 1
Q9NSD6
ID Q9NSD6 PRELIMINARY; PRT; 107 AA.
AC Q9NSD6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

```
RC   TISSUE=Lymphocytes;
RA   Hohmann A.;
RT   "Autoimmunity.";
RL   Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; L43092; AAA69746.2; -.
DR   HSSP; P01709; 2MCG.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     107    107
SQ   SEQUENCE   107 AA;  11306 MW;  A2B04B37187A5F00 CRC64;

  Query Match             93.0%;  Score 544;  DB 4;  Length 107;
  Best Local Similarity   96.3%;  Pred. No. 1.7e-47;
  Matches  103;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 ELTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIPDRFS 64
              |||||| |||||||||||:|||||||||||||||||||||||||||||||||||||||||
Db          1 ELTQDPVVSVALGQTVRITCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIPDRFS 60

Qy         65 GSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 111
              ||||||||||||||||||||||||||||||| ||||||:||||||
Db         61 GSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHAVFGGGTKLTVLG 107


RESULT 2
Q8TBC9
ID   Q8TBC9      PRELIMINARY;      PRT;   233 AA.
AC   Q8TBC9;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=B-cell;
RA   Strausberg R.;
RL   Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC022823; AAH22823.1; -.
DR   PIR; S12442; S12442.
DR   PIR; S30526; S30526.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   233 AA;  24867 MW;  367411BFD6F4DF92 CRC64;

  Query Match             74.9%;  Score 438;  DB 4;  Length 233;
  Best Local Similarity   75.2%;  Pred. No. 2.4e-36;
  Matches   82;  Conservative    9;  Mismatches   18;  Indels    0;  Gaps    0;

Qy          3 SSELTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIPDR 62
              | |||| |:|||: ||| |:|| ||:|   || ||||||||||||||  | ||||||:|
Db         20 SYELTQPPSVSVSPGQTARITCSGDALPKQYAYWYQQKPGQAPVLVIYKDNERPSGIPER 79

Qy         63 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 111
              ||||||| | :|||:| |||||||||| | |||| :|||||||:|||||
Db         80 FSGSSSGTTVTLTISGVQAEDEADYYCQSADSSGTYWVFGGGTKLTVLG 128


RESULT 3
Q8N5F4
ID   Q8N5F4      PRELIMINARY;      PRT;   233 AA.
AC   Q8N5F4;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain, and Lung;
RA   Strausberg R.;
RL   Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC032452; AAH32452.1; -.
DR   PIR; S12441; S12441.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   233 AA;  24961 MW;  F092CFB6AA6E3A9A CRC64;

  Query Match             73.0%;  Score 427;  DB 4;  Length 233;
  Best Local Similarity   73.4%;  Pred. No. 3.2e-35;
  Matches   80;  Conservative    9;  Mismatches   20;  Indels    0;  Gaps    0;

Qy          3 SSELTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIPDR 62
              | |||| |:|||: ||| |:|| ||:|   || ||||| || ||||||    |||||:|
Db         20 SYELTQPPSVSVSPGQTARITCSGDALPKKYAYWYQQKSGQTPVLVIYDDTERPSGIPER 79

Qy         63 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 111
              |||||||  |:|||::||| |||||||| | |||||||||||||:|||||
Db         80 FSGSSSGTVATLTLSGAQVEDEADYYCYSSDSSGNHWVFGGGTKLTVLG 128


RESULT 4
Q7Z2E8
ID   Q7Z2E8      PRELIMINARY;      PRT;    81 AA.
AC   Q7Z2E8;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Rearranged Vl3l segment (Rearranged Vl3l gene segment)
DE   (Fragment).
GN   VL3L.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Hodgkin lymphoma, and Mantle cell lymphoma;
RA   Tinguely M., Rosenquist R., Sundstroem C., Amini R.M., Kuppers R.,
RA   Hansmann M.L., Brauninger A.;
RT   "Analysis of a clonally related mantle cell and Hodgkin lymphoma
RT   indicates Epstein-Barr virus infection of a Hodgkin/Reed-Sternberg
RT   cell precursor in a germinal center.";
RL   Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ564423; CAD92030.1; -.
DR   EMBL; AJ564424; CAD92031.1; -.
FT   NON_TER       1      1
FT   NON_TER      81     81
SQ   SEQUENCE   81 AA;  8702 MW;  CFF1D4666B794C9F CRC64;
```

```
  Query Match             71.6%;  Score 419;  DB 4;  Length 81;
  Best Local Similarity   95.1%;  Pred. No. 5.5e-35;
  Matches   77;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         22 VTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIPDRFSGSSSGNTASLTITGAQA 81
              :|||||||||:||||||||||||||||||||:|||||||||||||||||||||||||||||
Db          1 ITCQGDSLRSFYASWYQQKPGQAPVLVIYGKSNRPSGIPDRFSGSSSGNTASLTITGAQA 60

Qy         82 EDEADYYCNSRDSSGNHWVFG 102
              ||||||||||||||||| |||
Db         61 EDEADYYCNSRDSSGNHMVFG 81


RESULT 5
Q8N355
ID   Q8N355      PRELIMINARY;      PRT;   234 AA.
AC   Q8N355;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Strausberg R.;
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC028090; AAH28090.1; -.
DR   PIR; S12441; S12441.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   234 AA;  24792 MW;  CC848CAEBA4A9D63 CRC64;

  Query Match             62.8%;  Score 367.5;  DB 4;  Length 234;
  Best Local Similarity   67.3%;  Pred. No. 3.4e-29;
  Matches   72;  Conservative   14;  Mismatches   20;  Indels    1;  Gaps    1;

Qy          6 LTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIPDRFSG 65
              ||| |:|||| ||| |:|| |::: |    |||||||||||||:|  ::||||||:||||
Db         23 LTQPPSVSVAPGQTARITCGGNNIGSKSVHWYQQKPGQAPVLVVYDDSDRPSGIPERFSG 82

Qy         66 SSSGNTASLTITGAQAEDEADYYCNSRDSSGNH-WVFGGGTELTVLG 111
              |:||||:|||:   | |||||||   ||| :|  ||||||:|||||
Db         83 SNSGNTATLTISRVDAGDEADYYCQLWDSSSDHPVVFGGGTKLTVLG 129


RESULT 6
Q9UL82
ID   Q9UL82      PRELIMINARY;      PRT;   107 AA.
AC   Q9UL82;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Myosin-reactive immunoglobulin light chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035032; AAD56268.1; -.
DR   HSSP; P01703; 7FAB.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     107    107
SQ   SEQUENCE   107 AA;  11445 MW;  52F0CC1AB26821DC CRC64;

  Query Match             62.6%;  Score 366.5;  DB 4;  Length 107;
  Best Local Similarity   67.6%;  Pred. No. 1.6e-29;
  Matches   73;  Conservative   10;  Mismatches   24;  Indels    1;  Gaps    1;

Qy          3 SSELTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIPDR 62
              | ||||  :|||: ||| |:|| || |   || |:||||||:|||:    ||||||:|
Db          1 SYELTQPSSVSVSPGQTARITCSGDLLAKKYARWFQQKPGQAPILVIFKDTERPSGIPER 60

Qy         63 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVL 110
              ||||||| | :|||:||| |||||||| |  |  |  ||||||:||||
Db         61 FSGSSSGTTVTLTISGAQVEDEADYYCYSA-SDNNGRVFGGGTKLTVL 107


RESULT 7
Q8WUK4
ID   Q8WUK4      PRELIMINARY;      PRT;   237 AA.
AC   Q8WUK4;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Tonsil;
RA   Strausberg R.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC020233; AAH20233.1; -.
DR   PIR; S12441; S12441.
DR   PIR; S12627; S12627.
DR   PIR; S29258; S29258.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   237 AA;  24897 MW;  73C7D70B8039D186 CRC64;

  Query Match             59.1%;  Score 346;  DB 4;  Length 237;
  Best Local Similarity   64.3%;  Pred. No. 5.1e-27;
  Matches   72;  Conservative    8;  Mismatches   28;  Indels    4;  Gaps    2;

Qy          4 SELTQDPAVSVALGQTVRVTCQGDSLR---SYYASWYQQKPGQAPVLVIYGKNNRPSGIP 60
              | ||| |:|| | || | ::| | |       |   |||| || || |:||| :|||||:|
Db         21 SVLTQPPSVSGAPGQRVTISCTGSSSNIGAGYDVHWYQQLPGTAPKLLIYGNSNRPSGVP 80

Qy         61 DRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSS-GNHWVFGGGTELTVLG 111
              |||||| || :||| ||| |||||||||| | |||     ||||||:|||||
Db         81 DRFSGSKSGTSASLAITGLQAEDEADYYCQSYDSSLSGFVVFGGGTKLTVLG 132
```

```
RESULT 8
Q8WTU6
ID   Q8WTU6      PRELIMINARY;      PRT;   237 AA.
AC   Q8WTU6;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Tonsil;
RA   Strausberg R.;
RL   Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC022098; AAH22098.1; -.
DR   PIR; S12441; S12441.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   237 AA;  24884 MW;  E6CF371E753968E8 CRC64;

  Query Match           58.1%;  Score 340;  DB 4;  Length 237;
  Best Local Similarity   62.6%;  Pred. No. 2.1e-26;
  Matches   72;  Conservative    9;  Mismatches   24;  Indels   10;  Gaps    3;

Qy          4 SELTQDPAVSVALGQTVRVTCQGDSLR---SYYASWYQQKPGQAPVLVIYGKNNRPSGIP 60
              | ||| |:|| | || | ::| | |       |   |||| || || |:||| :|||||:|
Db         21 SVLTQPPSVSGAPGQRVTISCTGSSSNIGAGYDVHWYQQLPGTAPKLLIYGNSNRPSGVP 80

Qy         61 DRFSGSSSGNTASLTITGAQAEDEADYYCNSRD----SSGNHWVFGGGTELTVLG 111
              |||||| || :||| ||| |||||||||| | |    :||   ||||||:|||||
Db         81 DRFSGSKSGTSASLAITGLQAEDEADYYCQSYDYSLSASG---VFGGGTKLTVLG 132


RESULT 9
Q96E61
ID   Q96E61      PRELIMINARY;      PRT;   236 AA.
AC   Q96E61;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Strausberg R.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC012876; AAH12876.1; -.
DR   PIR; S12440; S12440.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   236 AA;  24712 MW;  7EC9FB3622FED957 CRC64;

  Query Match           57.4%;  Score 335.5;  DB 4;  Length 236;
  Best Local Similarity   61.3%;  Pred. No. 5.9e-26;
  Matches   68;  Conservative   10;  Mismatches   30;  Indels    3;  Gaps    1;

Qy          4 SELTQDPAVSVALGQTVRVTCQGDSLR---SYYASWYQQKPGQAPVLVIYGKNNRPSGIP 60
              | | | |:|| | |||| ::| | |       |   |||| || || ::|||  |||||:|
Db         21 SVLAQPPSVSGAPGQTVTISCTGSSTNIGAGYAVHWYQQFPGAAPKVLIYGNYNRPSGVP 80

Qy         61 DRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 111
              |||||| || :||| ||| |||||||||| | | |  :  ||| ||::|||||
Db         81 DRFSGSKSGTSASLAITGLQAEDEADYYCQSYDGSLSGSVFGAGTKVTVLG 131


RESULT 10
Q7Z2U7
ID   Q7Z2U7      PRELIMINARY;      PRT;   234 AA.
AC   Q7Z2U7;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC054883; AAH54883.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   234 AA;  25015 MW;  9A5723ABC393A06F CRC64;

  Query Match           56.8%;  Score 332.5;  DB 4;  Length 234;
  Best Local Similarity   59.4%;  Pred. No. 1.2e-25;
  Matches   63;  Conservative   19;  Mismatches   23;  Indels    1;  Gaps    1;

Qy          6 LTQDPAVSVALGQTVRVTCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIPDRFSG 65
              ||| |:|||| |:| |:||  |:: :    |||||  ||||||::  |:||||||:||||
Db         23 LTQPPSVSVAPGKTARITCGADNIGAKSVHWYQQKTDQAPVLVVHDDNDRPSGIPERFSG 82

Qy         66 SSSGNTASLTITGAQAEDEADYYCNSRDSSGNH-WVFGGGTELTVL 110
              |:|||||:|:|:  :  |||||:|   |:||   |:|||||:||||
Db         83 SNSGNTATLSISRVEPGDEADYFCQVWDNSGGQLWMFGGGTKLTVL 128


RESULT 11
Q96JD0
ID   Q96JD0      PRELIMINARY;      PRT;   116 AA.
AC   Q96JD0;
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DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Amyloid lambda 6 light chain variable region SAR (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Bone marrow;
RA   Perfetti V., Casarini S., Colli Vignarelli M., Merlini G.;
RT   "Amyloid lambda 6 light chain variable region SAR.";
RL   Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF267875; AAK58587.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     116    116
SQ   SEQUENCE   116 AA;  12294 MW;  F7B0E9F49FAE369E CRC64;

  Query Match             55.2%;  Score 323;  DB 4;  Length 116;
  Best Local Similarity   59.1%;  Pred. No. 4.5e-25;
  Matches   65;  Conservative   15;  Mismatches   26;  Indels    4;  Gaps    2;

Qy          6 LTQDPAVSVALGQTVRVTCQGD--SLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIPDRF 63
              |||  :|| : |:|| ::| |    |: : |  ||| :|| ||  |||  | ||||:||||
Db          4 LTQPHSVSESPGKTVTISCTGSSGSIATNYVQWYQLRPGSAPTTVIYEDNQRPSGVPDRF 63

Qy         64 SGS--SSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 111
              |||  || |:|||||:| : |||||||| | |||  : :|||||:|||||
Db         64 SGSIDSSSNSASLTISGLKTEDEADYYCQSYDSSIGNVIFGGGTKLTVLG 113


RESULT 12
Q96JD1
ID   Q96JD1      PRELIMINARY;      PRT;   112 AA.
AC   Q96JD1;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Amyloid lambda 6 light chain variable region PIP (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Bone marrow;
RA   Perfetti V., Casarini S., Colli Vignarelli M., Merlini G.;
RT   "Amyloid lambda 6 light chain variable region PIP.";
RL   Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF267874; AAK58586.1; -.
DR   PIR; A30323; A30323.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     112    112
SQ   SEQUENCE   112 AA;  12047 MW;  0D3885AC23567B9F CRC64;

  Query Match             55.1%;  Score 322.5;  DB 4;  Length 112;
  Best Local Similarity   59.1%;  Pred. No. 4.9e-25;
  Matches   65;  Conservative   16;  Mismatches   24;  Indels    5;  Gaps    3;

Qy          6 LTQDPAVSVALGQTVRVTC--QGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIPDRF 63
              |||  :|| : |:|: ::|     |: | |  ||||:|| ||  |||  | ||||:||||
Db          4 LTQPHSVSESPGKTITISCTRSSGSIASNYVQWYQQRPGSAPTTVIYEDNQRPSGVPDRF 63

Qy         64 SGS--SSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVLG 111
              |||  || |:|||||:| : |||||||| | ||: |: :|||||:|||||
Db         64 SGSIDSSSNSASLTISGLKTEDEADYYCQSYDSN-NYALFGGGTQLTVLG 112


RESULT 13
Q8TE63
ID   Q8TE63      PRELIMINARY;      PRT;   110 AA.
AC   Q8TE63;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Immunglobulin light chain variable region (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95007525; PubMed=7923137;
RA   Hall B.L., Murray J.H., Haspel M.V., Kobrin B.J.;
RT   "Establishment, molecular rescue, and expression of 123AV16-1, a
RT   tumor-reactive human monoclonal antibody.";
RL   Cancer Res. 54:5178-5185(1994).
DR   EMBL; L33985; AAL68704.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     110    110
SQ   SEQUENCE   110 AA;  11479 MW;  599D1628F8F5437C CRC64;

  Query Match             54.5%;  Score 319;  DB 4;  Length 110;
  Best Local Similarity   58.7%;  Pred. No. 1.1e-24;
  Matches   64;  Conservative   13;  Mismatches   30;  Indels    2;  Gaps    1;

Qy          4 SELTQDPAVSVALGQTVRVTCQGDS--LRSYYASWYQQKPGQAPVLVIYGKNNRPSGIPD 61
              | ||| |:|| | || | ::| | |  : : : ||||| || || |:||  | ||||:||
Db          2 SALTQPPSVSAAPGQKVTISCSGTSSNIGNNFVSWYQQFPGTAPKLLIYDNNKRPSGVPD 61

Qy         62 RFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVL 110
              ||||| || :|:| ||| |  ||||||| : |:     ||||||:||||
Db         62 RFSGSKSGTSATLGITGLQTGDEADYYCGTWDTRLRAGVFGGGTKLTVL 110


RESULT 14
Q96JD2
ID   Q96JD2      PRELIMINARY;      PRT;   112 AA.
AC   Q96JD2;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Amyloid lambda 6 light chain variable region NEG (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Bone marrow;
RA   Perfetti V., Casarini S., Colli Vignarelli M., Merlini G.;
RT   "Amyloid lambda 6 light chain variable region NEG.";
RL   Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF267873; AAK58585.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
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FT   NON_TER     112    112
SQ   SEQUENCE   112 AA;  11908 MW;  080B4B37E2360B06 CRC64;

  Query Match             54.0%;  Score 316;  DB 4;  Length 112;
  Best Local Similarity   58.7%;  Pred. No. 2.2e-24;
  Matches   64;  Conservative   13;  Mismatches   28;  Indels    4;  Gaps    2;

Qy          6 LTQDPAVSVALGQTVRVTCQGDS--LRSYYASWYQQKPGQAPVLVIYGKNNRPSGIPDRF 63
              |||  :|| : |:|: ::| | |  : |    ||||:||:|| :|:|  | ||||:||||
Db          4 LTQPHSVSGSPGKTITISCTGSSGRIASNSVQWYQQRPGSAPNIVMYENNQRPSGVPDRF 63

Qy         64 SGS--SSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGGTELTVL 110
              |||  || |:||||:|   |||||||| | | | |  |||||| ||||
Db         64 SGSIDSSSNSASLTISGLMTEDEADYYCQSFDDSTNQGVFGGGTRLTVL 112


RESULT 15
Q8NEJ1
ID   Q8NEJ1      PRELIMINARY;      PRT;   236 AA.
AC   Q8NEJ1;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RA   Strausberg R.;
RL   Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC030984; AAH30984.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   236 AA;  25024 MW;  1703B77942630E08 CRC64;

  Query Match             52.7%;  Score 308.5;  DB 4;  Length 236;
  Best Local Similarity   57.3%;  Pred. No. 3.2e-23;
  Matches   63;  Conservative   15;  Mismatches   29;  Indels    3;  Gaps    2;

Qy          4 SELTQDPAVSVALGQTVRVTCQG--DSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIPD 61
              | ||| |: | : || | ::| |    :: | |  |||| || || |:||  : ||||:||
Db         21 SVLTQPPSASGSPGQRVTISCSGSRSNIGSNYVYWYQQVPGTAPKLLIYRNDQRPSGVPD 80

Qy         62 RFSGSSSGNTASLTITGAQAEDEADYYCNSRDSS-GNHWVFGGGTELTVL 110
              ||||| || :||| |:| ::|||||||| : | |   | ||||||:||||
Db         81 RFSGSKSGTSASLAISGLRSEDEADYYCAAWDDSLSVHVVFGGGTKLTVL 130


Search completed: September  9, 2004, 11:08:46
Job time : 37.1538 secs
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